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(21) International Application Number: PCT/US98/20775 (22) International Filing Date: 1 October 1998 (01.10.98) (30) Priority Data: <table border="0"><tr><td>60/060,837</td><td>2 October 1997 (02.10.97)</td><td>US</td></tr><tr><td>60/060,862</td><td>2 October 1997 (02.10.97)</td><td>US</td></tr><tr><td>60/060,839</td><td>2 October 1997 (02.10.97)</td><td>US</td></tr><tr><td>60/060,866</td><td>2 October 1997 (02.10.97)</td><td>US</td></tr><tr><td>60/060,843</td><td>2 October 1997 (02.10.97)</td><td>US</td></tr><tr><td>60/060,836</td><td>2 October 1997 (02.10.97)</td><td>US</td></tr><tr><td>60/060,838</td><td>2 October 1997 (02.10.97)</td><td>US</td></tr><tr><td>60/060,874</td><td>2 October 1997 (02.10.97)</td><td>US</td></tr><tr><td>60/060,833</td><td>2 October 1997 (02.10.97)</td><td>US</td></tr><tr><td>60/060,884</td><td>2 October 1997 (02.10.97)</td><td>US</td></tr><tr><td>60/060,880</td><td>2 October 1997 (02.10.97)</td><td>US</td></tr></table> (71) Applicant (for all designated States except US): HUMAN GENOME SCIENCES, INC. [US/US]; 9410 Key West Avenue, Rockville, MD 20850 (US). (72) Inventors; and (75) Inventors/Applicants (for US only): DUAN, D., Roxanne [US/US]; 5515 Northfield Road, Bethesda, MD 20817 (US). FLORENCE, Kimberly, A. [US/US]; 12805 At-		60/060,837	2 October 1997 (02.10.97)	US	60/060,862	2 October 1997 (02.10.97)	US	60/060,839	2 October 1997 (02.10.97)	US	60/060,866	2 October 1997 (02.10.97)	US	60/060,843	2 October 1997 (02.10.97)	US	60/060,836	2 October 1997 (02.10.97)	US	60/060,838	2 October 1997 (02.10.97)	US	60/060,874	2 October 1997 (02.10.97)	US	60/060,833	2 October 1997 (02.10.97)	US	60/060,884	2 October 1997 (02.10.97)	US	60/060,880	2 October 1997 (02.10.97)	US	(74) Agents: BROOKES, A., Anders et al.; Human Genome Sciences, Inc., 9410 Key West Avenue, Rockville, MD 20850 (US). (81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i> <i>With an indication in relation to deposited biological material furnished under Rule 13bis separately from the description.</i>	
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(54) Title: 101 HUMAN SECRETED PROTEINS																																				
(57) Abstract <p>The present invention relates to novel human secreted proteins and isolated nucleic acids containing the coding regions of the genes encoding such proteins. Also provided are vectors, host cells, antibodies, and recombinant methods for producing human secreted proteins. The invention further relates to diagnostic and therapeutic methods useful for diagnosis and treating disorders related to these novel human secreted proteins.</p>																																				

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101 Human Secreted Proteins

Field of the Invention

This invention relates to newly identified polynucleotides and the polypeptides encoded by these polynucleotides, uses of such polynucleotides and polypeptides, and
5 their production.

Background of the Invention

Unlike bacterium, which exist as a single compartment surrounded by a membrane, human cells and other eucaryotes are subdivided by membranes into many functionally distinct compartments. Each membrane-bounded compartment, or
10 organelle, contains different proteins essential for the function of the organelle. The cell uses "sorting signals," which are amino acid motifs located within the protein, to target proteins to particular cellular organelles.

One type of sorting signal, called a signal sequence, a signal peptide, or a leader sequence, directs a class of proteins to an organelle called the endoplasmic reticulum
15 (ER). The ER separates the membrane-bounded proteins from all other types of proteins. Once localized to the ER, both groups of proteins can be further directed to another organelle called the Golgi apparatus. Here, the Golgi distributes the proteins to vesicles, including secretory vesicles, the cell membrane, lysosomes, and the other organelles.

20 Proteins targeted to the ER by a signal sequence can be released into the extracellular space as a secreted protein. For example, vesicles containing secreted proteins can fuse with the cell membrane and release their contents into the extracellular space - a process called exocytosis. Exocytosis can occur constitutively or after receipt of a triggering signal. In the latter case, the proteins are stored in secretory vesicles (or
25 secretory granules) until exocytosis is triggered. Similarly, proteins residing on the cell membrane can also be secreted into the extracellular space by proteolytic cleavage of a "linker" holding the protein to the membrane.

Despite the great progress made in recent years, only a small number of genes encoding human secreted proteins have been identified. These secreted proteins include
30 the commercially valuable human insulin, interferon, Factor VIII, human growth hormone, tissue plasminogen activator, and erythropoietin. Thus, in light of the pervasive role of secreted proteins in human physiology, a need exists for identifying and characterizing novel human secreted proteins and the genes that encode them. This knowledge will allow one to detect, to treat, and to prevent medical disorders by using
35 secreted proteins or the genes that encode them.

Summary of the Invention

The present invention relates to novel polynucleotides and the encoded polypeptides. Moreover, the present invention relates to vectors, host cells, antibodies, and recombinant methods for producing the polypeptides and polynucleotides. Also provided are diagnostic methods for detecting disorders related to the polypeptides, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying binding partners of the polypeptides.

Detailed Description

Definitions

The following definitions are provided to facilitate understanding of certain terms used throughout this specification.

In the present invention, "isolated" refers to material removed from its original environment (e.g., the natural environment if it is naturally occurring), and thus is altered "by the hand of man" from its natural state. For example, an isolated polynucleotide could be part of a vector or a composition of matter, or could be contained within a cell, and still be "isolated" because that vector, composition of matter, or particular cell is not the original environment of the polynucleotide.

In the present invention, a "secreted" protein refers to those proteins capable of being directed to the ER, secretory vesicles, or the extracellular space as a result of a signal sequence, as well as those proteins released into the extracellular space without necessarily containing a signal sequence. If the secreted protein is released into the extracellular space, the secreted protein can undergo extracellular processing to produce a "mature" protein. Release into the extracellular space can occur by many mechanisms, including exocytosis and proteolytic cleavage.

As used herein, a "polynucleotide" refers to a molecule having a nucleic acid sequence contained in SEQ ID NO:X or the cDNA contained within the clone deposited with the ATCC. For example, the polynucleotide can contain the nucleotide sequence of the full length cDNA sequence, including the 5' and 3' untranslated sequences, the coding region, with or without the signal sequence, the secreted protein coding region, as well as fragments, epitopes, domains, and variants of the nucleic acid sequence. Moreover, as used herein, a "polypeptide" refers to a molecule having the translated amino acid sequence generated from the polynucleotide as broadly defined.

In the present invention, the full length sequence identified as SEQ ID NO:X was often generated by overlapping sequences contained in multiple clones (contig

analysis). A representative clone containing all or most of the sequence for SEQ ID NO:X was deposited with the American Type Culture Collection ("ATCC"). As shown in Table 1, each clone is identified by a cDNA Clone ID (Identifier) and the ATCC Deposit Number. The ATCC is located at 10801 University Boulevard,
5 Manassas, Virginia 20110-2209, USA. The ATCC deposit was made pursuant to the terms of the Budapest Treaty on the international recognition of the deposit of microorganisms for purposes of patent procedure.

A "polynucleotide" of the present invention also includes those polynucleotides capable of hybridizing, under stringent hybridization conditions, to sequences contained
10 in SEQ ID NO:X, the complement thereof, or the cDNA within the clone deposited with the ATCC. "Stringent hybridization conditions" refers to an overnight incubation at 42° C in a solution comprising 50% formamide, 5x SSC (750 mM NaCl, 75 mM sodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the
15 filters in 0.1x SSC at about 65°C.

Also contemplated are nucleic acid molecules that hybridize to the polynucleotides of the present invention at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation of formamide concentration (lower percentages
20 of formamide result in lowered stringency); salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37°C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH₂PO₄; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 ug/ml salmon sperm blocking DNA; followed by washes at 50°C with 1XSSPE, 0.1% SDS. In addition, to achieve even
25 lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5X SSC).

Note that variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. Typical blocking reagents include
30 Denhardt's reagent, BLOTTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

Of course, a polynucleotide which hybridizes only to polyA+ sequences (such
35 as any 3' terminal polyA+ tract of a cDNA shown in the sequence listing), or to a

complementary stretch of T (or U) residues, would not be included in the definition of "polynucleotide," since such a polynucleotide would hybridize to any nucleic acid molecule containing a poly (A) stretch or the complement thereof (e.g., practically any double-stranded cDNA clone).

5 The polynucleotide of the present invention can be composed of any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. For example, polynucleotides can be composed of single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and
10 double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, the polynucleotide can be composed of triple-stranded regions comprising RNA or DNA or both RNA and DNA. A polynucleotide may also contain one or more modified bases or DNA or RNA backbones modified for stability
15 or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications can be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically, or metabolically modified forms.

 The polypeptide of the present invention can be composed of amino acids joined
20 to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres, and may contain amino acids other than the 20 gene-encoded amino acids. The polypeptides may be modified by either natural processes, such as posttranslational processing, or by chemical modification techniques which are well known in the art. Such modifications are well described in basic texts and in more detailed monographs,
25 as well as in a voluminous research literature. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be
30 branched, for example, as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched, and branched cyclic polypeptides may result from posttranslation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a
35 nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine,

formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. (See, for instance, PROTEINS -
5 STRUCTURE AND MOLECULAR PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993); POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed., Academic Press, New York, pgs. 1-12 (1983); Seifter et al., Meth Enzymol 182:626-646 (1990);
10 Rattan et al., Ann NY Acad Sci 663:48-62 (1992).)

"SEQ ID NO:X" refers to a polynucleotide sequence while "SEQ ID NO:Y" refers to a polypeptide sequence, both sequences identified by an integer specified in Table 1.

"A polypeptide having biological activity" refers to polypeptides exhibiting
15 activity similar, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. In the case where dose dependency does exist, it need not be identical to that of the polypeptide, but rather substantially similar to the dose-dependence in a given activity as compared to the polypeptide of the present
20 invention (i.e., the candidate polypeptide will exhibit greater activity or not more than about 25-fold less and, preferably, not more than about tenfold less activity, and most preferably, not more than about three-fold less activity relative to the polypeptide of the present invention.)

25 Polynucleotides and Polypeptides of the Invention

FEATURES OF PROTEIN ENCODED BY GENE NO: 1

In specific embodiments, polypeptides of the invention comprise the following
30 amino acid sequence:
MLMKINFYPLPKPKLHTSISNCLLDISIYKPSSLISITSDLPGLTLKSXNFSPTPM
P GQNLVVTSYSSSLASSHPCSVQCWIL (SEQ ID NO:215). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in CD34 positive blood cells.

35 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are

not limited to, abnormalities of the immune system, in addition to reproductive disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g. immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of diseases and disorders of the immune system. Similarly, the expression of this gene product in immune cells indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immunodeficiency diseases such as AIDS, leukemia, rheumatoid arthritis, granulomatous disease, inflammatory bowel disease, sepsis, acne, neutropenia, neutrophilia, psoriasis, hypersensitivities, such as T-cell mediated cytotoxicity; immune reactions to transplanted organs and tissues, such as host-versus-graft and graft-versus-host diseases, or autoimmunity disorders, such as autoimmune infertility, lense tissue injury, demyelination, systemic lupus erythematosus, drug induced hemolytic anemia, rheumatoid arthritis, Sjogren's disease, scleroderma and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:11 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To

list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 538 of SEQ ID NO:11, b is an integer of 15 to 552, where both a and b correspond to the
5 positions of nucleotide residues shown in SEQ ID NO:11, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 2

10 This gene is expressed primarily in healing wound tissue, Hodgkin's lymphoma, and to a lesser extent, in other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are
15 not limited to, proliferative, immune, or hematopoietic disorders, particularly Hodgekin's lymphoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or
20 lower levels may be routinely detected in certain tissues and cell types (e.g.immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an
25 individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of Hodgekin's lymphoma and treatment of wounds. Expression within wounded tissue and other cellular sources marked by proliferating cells indicates that this protein may play a role
30 in the regulation of cellular division, and may show utility in the diagnosis and treatment of cancer and other proliferative disorders. Similarly, embryonic development also involves decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Protein, as well as, antibodies directed
35 against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these

sequences are related to SEQ ID NO:12 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1420 of SEQ ID NO:12, b is an integer of 15 to 1434, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:12, and where the b is greater than or equal to a + 14.

10

FEATURES OF PROTEIN ENCODED BY GENE NO: 3

The translation product of this gene was shown to have homology to the human M6 membrane glycoprotein which is thought to be important in myelination of central nervous system neurons during development (See Genbank Accession No.bb51137975). In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: LAPR FAFSQCSLAIMLTLLFQIHFLMILSSNWAYLKDASKMQAYQDIKAKEEQELQDIQ SRSKEQLNSYT (SEQ ID NO:216). Polynucleotides encoding these polypeptides are also encompassed by the invention.

20

This gene is expressed primarily in fetal brain, and to a lesser extent, in schizophrenic hypothalamus.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, developmental or neural disorders, particularly neurological and psychogenic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g. developmental, neural, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

35

The tissue distribution in neural tissues indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of certain neurological psychogenic disorders, including schizophrenia. Moreover, polynucleotides and polypeptides corresponding to this gene are useful for the

5 detection/treatment of neurodegenerative disease states, behavioural disorders, or inflammatory conditions such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, meningitis, encephalitis, demyelinating diseases, peripheral neuropathies, neoplasia, trauma, congenital malformations, spinal cord injuries, ischemia and infarction, aneurysms, hemorrhages, mania, dementia, paranoia,

10 obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses, autism, and altered behaviors, including disorders in feeding, sleep patterns, balance, and preception. In addition, Elevated expression of this gene product in regions of the brain indicates that it plays a role in normal neural function. Potentially, this gene product is involved in synapse formation, neurotransmission, learning, cognition,

15 homeostasis, or neuronal differentiation or survival. Moreover, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed

20 tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:13 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome.

25 Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1867 of SEQ ID NO:13, b is an integer of 15 to 1881, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:13, and where the b is greater than or equal to a + 14.

30

FEATURES OF PROTEIN ENCODED BY GENE NO: 4

It is likely that the open reading frame containing the predicted signal peptide

35 continues in the 5' direction. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence:

IRHEGGGQPFTSXPLEILFFLNGWYNATYFLLLELFIFLYKGVLLPYPTANLVLDV

V (SEQ ID NO:217), and/or MVHTRCSGHGDQGGEEVSRGLVLRGRMGITLP
LPILECRRLVSWADGPGLEDGTHWPYAELLAQMSVLKKSHTAFLRTTCPTN
SHWCG (SEQ ID NO:218). Polynucleotides encoding these polypeptides are also
encompassed by the invention. The gene encoding the disclosed cDNA is believed to
reside on chromosome 11. Accordingly, polynucleotides related to this invention are
useful as a marker in linkage analysis for chromosome 11.

This gene is expressed primarily in adult brain.

Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions which include, but are
not limited to, neural disorders, particularly neurodegenerative diseases. Similarly,
polypeptides and antibodies directed to these polypeptides are useful in providing
immunological probes for differential identification of the tissue(s) or cell type(s). For a
number of disorders of the above tissues or cells, particularly of the central nervous
system, expression of this gene at significantly higher or lower levels may be routinely
detected in certain tissues and cell types (e.g. neural, and cancerous and wounded
tissues) or bodily fluids (e.g. lymph, serum, plasma, urine, synovial fluid and spinal
fluid) or another tissue or cell sample taken from an individual having such a disorder,
relative to the standard gene expression level, i.e., the expression level in healthy tissue
or bodily fluid from an individual not having the disorder. Preferred epitopes include
those comprising a sequence shown in SEQ ID NO:116 as residues: Thr-17 to Lys-25.

The tissue distribution in adult brain indicates that polynucleotides and
polypeptides corresponding to this gene are useful for the diagnosis and treatment of
neurodegenerative diseases. Moreover, polynucleotides and polypeptides
corresponding to this gene are useful for the detection/treatment of behavioural
disorders, or inflammatory conditions such as Alzheimers Disease, Parkinsons Disease,
Huntingtons Disease, Tourette Syndrome, meningitis, encephalitis, demyelinating
diseases, peripheral neuropathies, neoplasia, trauma, congenital malformations, spinal
cord injuries, ischemia and infarction, aneurysms, hemorrhages, schizophrenia, mania,
dementia, paranoia, obsessive compulsive disorder, panic disorder, learning
disabilities, ALS, psychoses, autism, and altered behaviors, including disorders in
feeding, sleep patterns, balance, and preception. In addition, Elevated expression of
this gene product in regions of the brain indicates that it plays a role in normal neural
function. Potentially, this gene product is involved in synapse formation,
neurotransmission, learning, cognition, homeostasis, or neuronal differentiation or
survival. Moreover, the gene or gene product may also play a role in the treatment
and/or detection of developmental disorders associated with the developing embryo,

sexually-linked disorders, or disorders of the cardiovascular system. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence
5 databases. Some of these sequences are related to SEQ ID NO:14 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence
10 described by the general formula of a-b, where a is any integer between 1 to 1046 of SEQ ID NO:14, b is an integer of 15 to 1060, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:14, and where the b is greater than or equal to a + 14.

15 FEATURES OF PROTEIN ENCODED BY GENE NO: 5

The gene encoding the disclosed cDNA is believed to reside on chromosome 5. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 5.

20 This gene is expressed primarily in 12 week old early stage human and infant brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are
25 not limited to, neural or developmental disorders, particularly neurodegenerative conditions. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower
30 levels may be routinely detected in certain tissues and cell types (e.g. developmental, neural, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an
35 individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:117 as residues: Phe-20 to Arg-26.

The tissue distribution in neural and developmental tissues indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of neurodevelopmental diseases. Moreover, the polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states, behavioural disorders, or inflammatory conditions such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, meningitis, encephalitis, demyelinating diseases, peripheral neuropathies, neoplasia, trauma, congenital malformations, spinal cord injuries, ischemia and infarction, aneurysms, hemorrhages, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses, autism, and altered bahaviors, including disorders in feeding, sleep patterns, balance, and preception. In addition, Elevated expression of this gene product in regions of the brain indicates that it plays a role in normal neural function. Potentially, this gene product is involved in synapse formation, neurotransmission, learning, cognition, homeostasis, or neuronal differentiation or survival. Moreover, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:15 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1241 of SEQ ID NO:15, b is an integer of 15 to 1255, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:15, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 6

The translation product of this gene was shown to have homology to the conserved MAP kinase phosphatase which is known to be important as an antagonist in MAP kinase activation (See Genbank Accession No.gil1050849). As such, a role in development or in cellular metabolism may be anticipated. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence:

RVIRLTXRANWSSTAVAAALELVDPPGCRNSARVKYCVVYDNNSSSTLEILLKD
 DDDSDSDGDGKDLVPQAAIEYGRILTRLTHHPVYILKGGYERFSGTYH
 FLRTQKIWMPQELDAFQPYPIEIVPGKVFVGNFSQACDPKIQKDLKIKAHV
 NVSMDTGPPFAGDADKLLHIRIEDSPEAQILPFLRHMCHFIEIHHHLGSVILIFST
 5 QGISRSCAIIAYLMHSNEQTLQRSWAYVKKCKNNMCPNRGLVSQLEWE
 KTILGDSITNIMDPLY (SEQ ID NO:219). Polynucleotides encoding these

polypeptides are also encompassed by the invention. The gene encoding the disclosed cDNA is believed to reside on chromosome 7. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 7.

10 This gene is expressed primarily in fetal kidney, liver, and spleen.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, developmental, immune, or haemopoietic disorders. Similarly,
 15 polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the haemopoietic system or developing immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types
 20 (e.g. developmental, renal, immune, hematopoietic, hepatic, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, bile, amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the
 25 disorder.

The tissue distribution in fetal liver, combined with the homology to a signal transduction regulatory protein indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of hematopoietic disorders involving blood stem cell formation, such as anemia, pancytopenia,
 30 leukopenia, thrombocytopenia or leukemia since stromal cells are important in the production of cells of hematopoietic lineages. The uses include bone marrow cell ex vivo culture, bone marrow transplantation, bone marrow reconstitution, radiotherapy or chemotherapy of neoplasia. The gene product may also be involved in lymphopoiesis, therefore, it can be used in immune disorders such as infection, inflammation, allergy,
 35 immunodeficiency etc. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies

directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:16 and may have been publicly available

5 prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1022 of SEQ ID NO:16, b

10 is an integer of 15 to 1036, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:16, and where the b is greater than or equal to a + 14.

15 FEATURES OF PROTEIN ENCODED BY GENE NO: 7

In specific embodiments, polypeptides of the invention comprise the following amino acid sequence:

IRHEFTSEKSWKSSCNEGESSSTSYMHQSPGGPTKLEIISDCNWEEDRNKILS

20 ILSQHINSNMPQSLKVGSIIELASQRKSRGEKNPPVYSSRVXISMPCQDQ

DDMAEKSGSETPDGPLSPGKMEDISPVQTDALDSVRERLHGGKGLPFY

AGLSPAGKLVAYKRKPSSSTGLIQVRIIFNLGIAPLYTPR (SEQ ID NO:220).

Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in human fetal heart.

25 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, developmental or cardiovascular disorders, particularly fetal cardiac defects. Similarly, polypeptides and antibodies directed to these polypeptides are useful

30 in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the cardiac system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g. developmental, cardiac, musculoskeletal, and cancerous and wounded tissues) or bodily fluids (e.g. lymph,

35 amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard

gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of fetal cardiac defects. Similarly, expression within fetal tissue indicates that this protein may play a role in the regulation of cellular division, and may show utility in the diagnosis and treatment of cancer and other proliferative disorders. Similarly, embryonic development also involves decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:17 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1000 of SEQ ID NO:17, b is an integer of 15 to 1014, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:17, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 8

It is likely that the open reading frame containing the predicted signal peptide continues in the 5' direction. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: CNIEYIRSDKCMFKHELEELRTTI (SEQ ID NO:221). Polynucleotides encoding these polypeptides are also encompassed by the invention. The gene encoding the disclosed cDNA is believed to reside on chromosome 2. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 2.

This gene is expressed primarily in fetal cochlea, other fetal tissues, and to a lesser extent in placenta.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are

not limited to, developmental disorders, particularly of auditory tissues. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the fetal developmental systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g. developmental, auditory, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, amniotic fluid, cochlear fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:120 as residues: Met-1 to His-6, Glu-33 to Asn-43.

The tissue distribution within fetal tissue indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of fetal developmental disorders, particularly of auditory tissues. Similarly, expression within fetal tissues and other cellular sources marked by proliferating cells indicates that this protein may play a role in the regulation of cellular division, and may show utility in the diagnosis and treatment of cancer and other proliferative disorders. Similarly, embryonic development also involves decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:18 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1273 of SEQ ID NO:18, b is an integer of 15 to 1287, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:18, and where the b is greater than or equal to a + 14.

35 FEATURES OF PROTEIN ENCODED BY GENE NO: 9

This gene is expressed primarily in nine week old early stage human.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, fetal developmental disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the fetal developmental systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g. developmental, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:121 as residues: Met-1 to Arg-6.

The tissue distribution in fetal tissue indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of some types of fetal developmental disorders. Moreover, the expression within embryonic tissue indicates that this protein may play a role in the regulation of cellular division, and may show utility in the diagnosis and treatment of cancer and other proliferative disorders. Similarly, embryonic development also involves decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:19 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1091 of SEQ ID NO:19, b is an integer of 15 to 1105, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:19, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 10

This gene is expressed primarily in epididymus.

- 5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, reproductive disorders, particularly male sterility. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing
- 10 immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the male reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g. reproductive, cancerous and wounded tissues) or bodily fluids (e.g. lymph, seminal fluid, serum, plasma, urine, synovial fluid
- 15 and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- The tissue distribution in epididymus indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of
- 20 male sterility, and/or could be used as a male contraceptive. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:20 and may have been
- 25 publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence
- 30 described by the general formula of a-b, where a is any integer between 1 to 1075 of SEQ ID NO:20, b is an integer of 15 to 1089, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:20, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 11

35

The translation product of this gene shares sequence homology with a mitotic phosphoprotein which is thought to be important in initiating and coordinating cell

division processes. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: HHQQVPEXDREDSPERCSDXXEEKKARRGRS PKGEFKDEEETVTTKHHITQATETTTTRHKRTANPSKTIDLGAAAHYTGDKAS PD QNASTHTPQSSVKTSVPSSKSSGDLVDLFDGTSQCNRRXS (SEQ ID NO:222), VSSDSVGGFRYSERYDPEPKSKWDEEWDKNKSAFPFSDKL GELSDKIGSTIDDTISKFRXKIEKTLQKDA ATXXRKRKREEADLPKVNSK MKRRL (SEQ ID NO:223), and/or RQSIFISHRPQRPPQPD TSAQQILPKP LILEQQHITQGTKQVQI R (SEQ ID NO:224). Polynucleotides encoding these polypeptides are also encompassed by the invention. The gene encoding the disclosed cDNA is believed to reside on chromosome 5. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 5.

This gene is expressed primarily in placenta, and to a lesser extent in T-cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, spontaneous abortion and in utero developmental problems, in addition to immune disorders, such as autoimmune conditions. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and reproductive systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g. developmental, immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:123 as residues: Ser-65 to Gly-71, Ser-155 to Leu-160, Gln-168 to Asp-179, Leu-189 to Pro-196, Gln-210 to Ser-218, Gln-224 to Pro-231, Val-326 to Asp-331.

The tissue distribution in placental tissue combined with the homology to mitotic phosphoprotein indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of diseases that arise in utero due to cell division abnormalities during fetal development. Alternatively, expression within T-cells indicates that the secreted protein may also be used to determine biological activity, to raise antibodies, as tissue markers, to isolate cognate ligands or receptors, to identify agents that modulate their interactions and as nutritional supplements. It may also have a

very wide range of biological activities. Typical of these are cytokine, cell proliferation/differentiation modulating activity or induction of other cytokines; immunostimulating/immunosuppressant activities (e.g. for treating human immunodeficiency virus infection, cancer, autoimmune diseases and allergy); regulation of hematopoiesis (e.g. for treating anaemia or as adjunct to chemotherapy); stimulation or growth of bone, cartilage, tendons, ligaments and/or nerves (e.g. for treating wounds, stimulation of follicle stimulating hormone (for control of fertility); chemotactic and chemokinetic activities (e.g. for treating infections, tumors); hemostatic or thrombolytic activity (e.g. for treating haemophilia, cardiac infarction etc.); anti-inflammatory activity (e.g. for treating septic shock, Crohn's disease); as antimicrobials; for treating psoriasis or other hyperproliferative diseases; for regulation of metabolism, and behaviour. Also contemplated is the use of the corresponding nucleic acid in gene therapy procedures. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:21 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2817 of SEQ ID NO:21, b is an integer of 15 to 2831, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:21, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 12

The translation product of this gene shares sequence homology with murine counterpart of the human TB2/DP1 which is thought to be important in familial adenomatous polyposis (FAP) disease as one of six genes deleted. Triggering of murine mast cells by IgE plus antigen results in a decrease of TB2/DP1 mRNA up to 60% after 2 h implying a possible role of this gene in regulation of the allergic effector cell. Reverse transcription-polymerase chain reaction (RT-PCR) analysis shows an ubiquitous expression pattern in a number of mouse cell lines and tissues. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: DQDGLRAVAALTLHQGRQLLYRK FVHPSLSRHEKEIDAYTVQAKE RSYETVLSFGKRGLNIAASAAVQAATXSQ GALAGRLRSFSMQDLRSISDAPAPA

YHDPYLEDQVSHRRPPIGYRAGGLQSDTEDECWSDTEAVPRAPARPRE
KPLIRSQSLRVVKKPPVREGTSRSLKVR TXKKTVPSDVDS (SEQ ID NO:225).

Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in T cells, and to a lesser extent, in fetal skin.

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer, particularly familial polyptosis, or other proliferating disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in
10 providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the colon, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g. immune, developmental tissues, integumentary, and cancerous and wounded tissues) or bodily fluids (e.g. lymph,
15 amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:124 as residues: Met-99 to Ala-114.

20 The tissue distribution in T-cells and fetal skin, combined with the homology to the DP1 gene of the FAP locus indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of familial adenomatous polyposis, as well as other cancers. It may also be useful in treating allergic disorders. Expression within fetal tissue and other cellular sources marked by
25 proliferating cells indicates that this protein may play a role in the regulation of cellular division, and may show utility in the diagnosis and treatment of cancer and other proliferative disorders. Similarly, embryonic development also involves decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in
30 cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:22 and may have been publicly available prior to conception of the present
35 invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more

polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1434 of SEQ ID NO:22, b is an integer of 15 to 1448, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:22, and where the b is greater than or equal to a + 14.

5

FEATURES OF PROTEIN ENCODED BY GENE NO: 13

The translation product of this gene shares sequence homology with a murine oligodendrocyte-specific protein related to peripheral myelin protein-22 (PMP-22).

- 10 PMP-22 is important in peripheral myelination and Schwann cell proliferation, and mutations in its gene cause diseases of peripheral nerves. Myelin plays a critical role in nervous system function and alterations in myelin-specific proteins cause a variety of neurologic disorders. The polynucleotide sequence of this gene may have a frame shift. Therefore the preferred signal peptide may reside in a frame other than the associated
- 15 polynucleotides of the above referenced gene. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence:

LCHRLPGRLQLLGVPVHAGPLWVYSGLPGTHDHRHPPGLPRPLAXHX
GPALHQHWGPGALQESQAGGXRRGPPHSGRYLRDGGXLLVRFNITRDFFDPL
YPGTKYELGPXYLGWSASLXSILGGLCLCSACCCGSEDEDQPPAPGGP

- 20 TXLPCP (SEQ ID NO:226). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in endothelial and T cells.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
- 25 biological sample and for diagnosis of diseases and conditions which include, but are not limited to, neurological disorders related to myelin abnormalities, in addition to immune or endothelial disorders, particularly vascular conditions. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a
- 30 number of disorders of the above tissues or cells, particularly of the nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g. neural, immune, vascular, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a
- 35 disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in immune cells combined with the homology to an oligodendrocyte-specific protein related to PMP-22 indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of diseases of the nervous system, particularly those involving aberrant myelination of the nerves, such as ALS and multiple sclerosis, or autoimmune disorders affecting neural tissues. Similarly, polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states, behavioural disorders, or inflammatory conditions such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, meningitis, encephalitis, demyelinating diseases, peripheral neuropathies, neoplasia, trauma, congenital malformations, spinal cord injuries, ischemia and infarction, aneurysms, hemorrhages, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, psychoses, autism, and altered behaviors, including disorders in feeding, sleep patterns, balance, and preception. In addition, elevated expression of this gene product in regions of the brain indicates that it plays a role in normal neural function. Potentially, this gene product is involved in synapse formation, neurotransmission, learning, cognition, homeostasis, or neuronal differentiation or survival. Moreover, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:23 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1197 of SEQ ID NO:23, b is an integer of 15 to 1211, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:23, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 14

The translation product of this gene shares high sequence homology at the nucleotide level with the human G protein-coupled receptor (EBI 1) gene, exon 1. This

EBI1 gene is a lymphoid-specific member of the G-protein-coupled receptor family. This receptor, also reported as the Epstein-Barr-induced cDNA EBI1, is expressed in normal lymphoid tissues and in several B- and T-lymphocyte cell lines. While the function and the ligand for EBI1 remain unknown, its sequence and gene structure
5 suggest that it is related to the receptors that recognize chemoattractants, such as interleukin-8, RANTES, C5a, and fMet-Leu-Phe. Like the chemoattractant receptors, EBI1 contains intervening sequences near its 5' end; however, EBI1 is unique in that both of its introns interrupt the coding region of the first extracellular domain. The gene is encoded on human chromosome 17q12-q21.2. None of the other G-protein-coupled
10 receptors has been mapped to this region, but the C-C chemokine family has been mapped to 17q11-q21. The mouse EBI1 cDNA has also been isolated and encodes a protein with 86% identity to the human homolog. .

This gene is expressed primarily in spinal cord.

Therefore, polynucleotides and polypeptides of the invention are useful as
15 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, inflammatory disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above
20 tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. neural, immune, skeletal, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the
25 standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to the EBI-1 gene indicates that polynucleotides and polypeptides corresponding to this gene are useful for developing diagnostics and small molecule therapeutics for affecting the action of chemoattractants
30 similar to interleukin-8, RANTES, C5a, and fMet-Leu-Phe. In turn, this could be useful in the treatment of inflammatory diseases such as sepsis, inflammatory bowel syndrome, psoriasis, and rheumatoid arthritis. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences,
35 are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:24 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are

specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1046 of SEQ ID NO:24, b
5 is an integer of 15 to 1060, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:24, and where the b is greater than or equal to a + 14.

10 FEATURES OF PROTEIN ENCODED BY GENE NO: 15

This gene is expressed primarily in osteoclastoma, and to a lesser extent, in T cell and fetal liver.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
15 biological sample and for diagnosis of diseases and conditions which include, but are not limited to, osteoclastoma; hematopoietic disorders; immune dysfunction; susceptibility to infection; or osteoporosis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of
20 the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g.skeletal tissues, immune or hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder,
25 relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in hematopoietic cells and tissues indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and/or treatment of disorders of the hematopoietic system. In particular, the
30 elevated expression of this gene product in osteoclastoma indicates that it may play a role particularly in the development of the osteoclast lineage, and thus may be particularly useful in conditions such as osteoporosis and osteopetrosis. Additionally, it may play more generalized roles in hematopoiesis, as evidenced by expression in T cells and fetal liver. Thus, it may also be used to affect the proliferation, survival,
35 activation, and/or differentiation of a variety of hematopoietic lineages. Thus, it may play roles in a variety of disease conditions, including lymphoma/leukemias; defects in immune modulation or immune surveillance; susceptibility to infection; and other

hematopoietic disorders. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:25 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1043 of SEQ ID NO:25, b is an integer of 15 to 1057, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:25, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 16

15

The translation product of this gene shares sequence homology with bup, a gene locus in mouse of unknown function. Retroviral insertions into this region (that also contains the bmi gene) are frequently correlated with lymphomagenesis (See Genbank Accession No. bbsl125119). The gene encoding the disclosed cDNA is believed to reside on chromosome 10. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 10.

This gene is expressed primarily in WI 38 lung fibroblasts, fetal lung, placenta, and to a lesser extent, in T cell lymphoma, fetal liver, and stromal cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, T cell lymphoma, fibrosis, mesenchymal disorders; respiratory disorders; ARDS. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the skeletal, respiratory, and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g. skeletal, pulmonary, immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, pulmonary surfactant and sputum, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the

disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:128 as residues: Gly-74 to Leu-83, Cys-90 to Arg-96, Glu-103 to Asn-109, Glu-133 to Gln-140, Gln-156 to Pro-164, Lys-183 to Arg-191.

5 The tissue distribution in lung tissue and cells indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and/or treatment of disorders of the lung and, more generally, of mesenchymal cells. Expression of this gene product is elevated in lung, as well as in a cell line derived from lung, suggesting a role in lung function. It is also elevated in mesenchymally-derived cells and tissues such as fibroblasts and endothelium. The expression of this gene also correlates with
10 lymphoma, and it is expressed at hematopoietic sites, such as fetal liver. Thus, it may also play a role in hematopoiesis, either in the survival, proliferation, and/or differentiation of various blood cell lineages. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences,
15 are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:26 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention
20 are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 966 of SEQ ID NO:26, b is an integer of 15 to 980, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:26, and where the b is greater than or equal to a + 14.

25 FEATURES OF PROTEIN ENCODED BY GENE NO: 17

This gene is expressed primarily in a breast cancer cell line and in Wilm's tumor samples, and to a lesser extent, in apoptotic and helper T cells, as well as activated macrophages.

30 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, breast cancer; wilm's tumor; hematopoietic disorders; immune dysfunction; acute renal failure. Similarly, polypeptides and antibodies directed to these
35 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the breast, kidney, and immune system, expression of this gene at

significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. breast, reproductive, immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, breast milk, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in proliferating tissues and cells indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and/or treatment of cancer. This gene product is expressed at elevated levels in both breast cancer cells as well as Wilm's tumor. This observation indicates that this gene product may play a role in the control of cell proliferation and/or survival, particularly since it is also observed in apoptotic T cells. Alternately, it may control other aspects of cell behavior or activation, as it is also observed in helper T cells and activated macrophages. Thus, it may play general roles in the immune system as well, either in the control of blood cell survival, proliferation, differentiation, or activation. Thus, this gene product may be useful in controlling immune modulation and immune surveillance as well. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:27 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 741 of SEQ ID NO:27, b is an integer of 15 to 755, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:27, and where the b is greater than or equal to a + 14.

30 FEATURES OF PROTEIN ENCODED BY GENE NO: 18

This gene is expressed primarily in the synovium.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, skeletal disorders, particularly joint disorders such as rheumatoid arthritis. Similarly, polypeptides and antibodies directed to these polypeptides are useful

in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the skeletal system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g. skeletal, synovium, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

10 The tissue distribution in the synovium indicates that the gene and protein product of this gene is useful for diagnosis of disorders of the joints as dysregulation of genes encoding proteins secreted from synovial tissues is thought to affect normal function of the joints and may lead to autoimmune disorders such as rheumatoid arthritis, lupus, scleroderma, and dermatomyositis as well as dwarfism, spinal deformation, and specific joint abnormalities as well as chondrodysplasias (ie. spondyloepiphyseal dysplasia congenita, familial osteoarthritis, Atelosteogenesis type II, metaphyseal chondrodysplasia type Schmid). Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:28 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 932 of SEQ ID NO:28, b is an integer of 15 to 946, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:28, and where the b is greater than or equal to a + 14.

30 **FEATURES OF PROTEIN ENCODED BY GENE NO: 19**

This gene is expressed primarily in amniotic cells, and to a lesser extent, in chronic lymphocytic leukemia cells of the spleen.

35 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, developmental or immune disorders, particularly leukemia. Similarly,

polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g. developmental, immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in leukemia cells indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment or diagnosis of leukemia and other immune diseases. Similarly, this gene product may be useful in the regulation of the proliferation; survival; differentiation; and/or activation of hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immunodeficiency diseases such as AIDS, leukemia, rheumatoid arthritis, granulomatous disease, inflammatory bowel disease, sepsis, acne, neutropenia, neutrophilia, psoriasis, hypersensitivities, such as T-cell mediated cytotoxicity; immune reactions to transplanted organs and tissues, such as host-versus-graft and graft-versus-host diseases, or autoimmunity disorders, such as autoimmune infertility, lense tissue injury, demyelination, systemic lupus erythematosus, drug induced hemolytic anemia, rheumatoid arthritis, Sjogren's disease, scleroderma and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:29 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more

polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 957 of SEQ ID NO:29, b is an integer of 15 to 971, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:29, and where the b is greater than or equal to a + 14.

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FEATURES OF PROTEIN ENCODED BY GENE NO: 20

The translation product of this gene was found to have homology to the human protein, defender against cell death 1 gene, which is a known antagonist of apoptosis (See Genseq Accession No:P46966). The gene encoding the disclosed cDNA is
10 believed to reside on chromosome 14. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 14.

This gene is expressed primarily in breast, lung, testes, B cells and T cells.

Therefore, polynucleotides and polypeptides of the invention are useful as
15 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, immune or pulmonary disorders, particularly cancer of the breast, lung, testes and B cells. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the
20 tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.immune, reproductive, pulmonary, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, breast milk, pulmonary surfactant or sputum, serum, plasma, urine,
25 synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
30 corresponding to this gene are useful for the diagnosis and treatment of cancer, particularly of the breast, lung, or in B-cell lymphoma. Similarly, expression within cellular sources marked by proliferating cells, combined with its homology to a conserved regulatory protein of apoptosis indicates that this protein may play a role in the regulation of cellular division, and may show utility in the diagnosis and treatment
35 of cancer and other proliferative disorders. Similarly, developmental tissues rely on decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be

useful in cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:30 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 994 of SEQ ID NO:30, b is an integer of 15 to 1008, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:30, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 21

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The translation product of this gene shares sequence homology with human and murine surface glycoprotein which is thought to be important in cell-cell interactions and transducing cellular signals (See Genseq Accession No.gil2997741).

This gene is expressed primarily in testis.

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Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, male reproductive diseases or disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the male reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.reproductive, immune, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, seminal fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:133 as residues: Thr-6 to Leu-11.

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The tissue distribution in testes combined with the homology to a conserved cell surface glycoprotein indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating and diagnosis of diseases associated with male reproductive system. Protein, as well as, antibodies directed against the protein may

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show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:31 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 976 of SEQ ID NO:31, b is an integer of 15 to 990, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:31, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 22

The translation product of this gene was found to have homology to the human myosin regulatory light chain which is thought to be important in muscle function (See Genbank Accession No.gil189013). In specific embodiments, polypeptides of the invention comprise the following amino acid sequence:

VDQMFQFASIDVAGNLDYKALSYVITHGEEKEE (SEQ ID NO:227), and/or
IRHEAYVILAVCLGG (SEQ ID NO:228). Polynucleotides encoding these polypeptides are also encompassed by the invention. The gene encoding the disclosed cDNA is believed to reside on chromosome 4. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 4.

This gene is expressed primarily in lung, testis, and macrophage.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancers and immune disorders, particularly afflicting the pulmonary or reproductive system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system and male reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.immune, pulmonary, reproductive, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, pulmonary surfactant or sputum, seminal fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression

level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:134 as residues: Tyr-47 to Phe-54, Arg-144 to Ser-149, Thr-152 to Asp-161, Glu-194 to Asn-203, Glu-242 to Pro-250, Thr-258 to Gly-263, Ala-269 to Gly-274.

The tissue distribution in immune cells and lung tissue indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of diseases of the immune system and male reproductive system. Alternatively, the homology to the conserved myosin regulatory light chain indicates that the protein product of this gene may be useful in the detection, treatment, and/or prevention of a variety of skeletal or cardiac muscle disorders, such as muscular sclerosis. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:32 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1117 of SEQ ID NO:32, b is an integer of 15 to 1131, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:32, and where the b is greater than or equal to a + 14.

25 FEATURES OF PROTEIN ENCODED BY GENE NO: 23

The translation product of this gene shares sequence homology with potassium channel regulatory subunit which is thought to be important in potassium ion regulation. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence:

WIQRIRHETNPKCSYIPPCKRENQKNLESVMNWQQYWKDEIGS
QPFTCYFNQHQRPDVLLHRTHEIVLLHCFLWPLVTFVVGVLIVLTICAKSL
AVKAEAMXEAQVLLKGKEACRKQSTEAVLIGTRPPAEPVFPAGDQGQHD
RALRGSSLSGNRRNRHNWKTWNLKACIPSAVAMAKGS RS (SEQ ID NO:229).

Polynucleotides encoding these polypeptides are also encompassed by the invention. The gene encoding the disclosed cDNA is believed to reside on chromosome 12.

Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 12.

This gene is expressed primarily in the brain.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, neural disorders, particularly neurodegenerative disorders, such as Alzheimers Disease, Parkinsons Disease, or Huntingtons Disease. Similarly,
10 polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. neural, cancerous and wounded tissues) or bodily fluids (e.g. lymph, serum, plasma, urine, synovial fluid and spinal fluid) or
15 another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in neural tissue combined with the homology to a potassium channel regulatory subunit indicates that polynucleotides and polypeptides
20 corresponding to this gene are useful for the diagnosis and treatment of diseases related to potassium channel malfunction in the brain. Similarly, polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states, behavioural disorders, or inflammatory conditions such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome,
25 meningitis, encephalitis, demyelinating diseases, peripheral neuropathies, neoplasia, trauma, congenital malformations, spinal cord injuries, ischemia and infarction, aneurysms, hemorrhages, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses, autism, and altered behaviors, including disorders in feeding, sleep patterns, balance, and
30 preception. In addition, elevated expression of this gene product in regions of the brain indicates that it plays a role in normal neural function. Potentially, this gene product is involved in synapse formation, neurotransmission, learning, cognition, homeostasis, or neuronal differentiation or survival. Moreover, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the
35 developing embryo, sexually-linked disorders, or disorders of the cardiovascular system. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many

polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:33 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1279 of SEQ ID NO:33, b is an integer of 15 to 1293, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:33, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 24

The translation product of this gene shares sequence homology with oxidoreductase which is thought to be important in inflammatory reactions.

This gene is expressed primarily in human pancreas tumor.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, metabolic or immune disorders, particularly proliferative conditions such as pancreas tumor. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. metabolic tissues, immune, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, bile, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:136 as residues: Ile-72 to Asn-77, Asp-98 to Val-105, Val-210 to Ile-216.

The tissue distribution in pancreatic tissue combined with the homology to oxidoreductase indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis of pancreas tumor and inflammatory diseases. Similarly, expression within cellular sources marked by proliferating cells indicates that this protein may play a role in the regulation of cellular division, and may show utility in the

diagnosis and treatment of cancer and other proliferative disorders. Similarly, developmental tissues rely on decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:34 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1000 of SEQ ID NO:34, b is an integer of 15 to 1014, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:34, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 25

The translation product of this gene was shown to have homology to the rat TIP120, which is thought to be important in the regulation of basal as well as activated transcriptional metabolism (See Genbank Accession No. gnllPID1014122). Based upon homology to the referenced gene, it is likely that the open reading frame containing the predicted signal peptide continues in the 5' direction. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence:

HYEKVRLQVPIRNSRVDPRVXKFTISDHPQPIDPLLKNCIGDFLKTLEDPDLNVR
RVALVTFNSAAHNKPSLIRDLLDTVLPHLYNETKVRKELIREVEMGPFK
HTVDDGLDIRKAAFECMYTLLDSCDLRLDIF EFLNHVEDGLKDHYDIK (SEQ ID
NO:230). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in infant brain and various cancers.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, neural or developmental disorders, particularly cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing

immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous or immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. developmental, neural, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:137 as residues: Ser-41 to Lys-53, Ser-80 to Pro-86, Ile-95 to Ser-110.

The tissue distribution in brain indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of a variety of neural disorders. Similarly, polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states, behavioural disorders, or inflammatory conditions such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, meningitis, encephalitis, demyelinating diseases, peripheral neuropathies, neoplasia, trauma, congenital malformations, spinal cord injuries, ischemia and infarction, aneurysms, hemorrhages, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses, autism, and altered bahaviors, including disorders in feeding, sleep patterns, balance, and preception. In addition, elevated expression of this gene product in regions of the brain indicates that it plays a role in normal neural function. Potentially, this gene product is involved in synapse formation, neurotransmission, learning, cognition, homeostasis, or neuronal differentiation or survival. Moreover, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:35 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1208 of SEQ ID NO:35, b is an integer of 15 to 1222, where

both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:35, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 26

5

It is likely that the open reading frame containing the predicted signal peptide continues in the 5' direction. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence:

IRHEHLRGVQERVNLSAPLLPKEDPIFTYLSKRLGRSIDDIGHLIHEGLQKNTSS
10 WVLYNMAFYWRIKN EPYQVVECA (SEQ ID NO:231). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in brain, testes and Hodgkins lymphoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
15 biological sample and for diagnosis of diseases and conditions which include, but are not limited to, neural, reproductive, or immune disorders, particularly Hodgkins lymphoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of
20 the immune system expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. neural, reproductive, immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, seminal fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard
25 gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:138 as residues: Ser-7 to Asp-13, Gln-93 to Leu-99, Ser-105 to His-122, Arg-125 to Thr-132.

The tissue distribution indicates that polynucleotides and polypeptides
30 corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in Hodgkins lymphoma indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other
35 processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also

used as an agent for immunological disorders including arthritis, asthma, immunodeficiency diseases such as AIDS, leukemia, rheumatoid arthritis, granulomatous disease, inflammatory bowel disease, sepsis, acne, neutropenia, neutrophilia, psoriasis, hypersensitivities, such as T-cell mediated cytotoxicity; immune reactions to transplanted organs and tissues, such as host-versus-graft and graft-versus-host diseases, or autoimmunity disorders, such as autoimmune infertility, lense tissue injury, demyelination, systemic lupus erythematosus, drug induced hemolytic anemia, rheumatoid arthritis, Sjogren's disease, scleroderma and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types including reproductive or neural tissues. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:36 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 887 of SEQ ID NO:36, b is an integer of 15 to 901, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:36, and where the b is greater than or equal to a + 14.

25 FEATURES OF PROTEIN ENCODED BY GENE NO: 27

It is likely that the sequence of this polynucleotide continues upstream of the preferred signal peptide. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence:

30 EFGTSPHQTCGRRPGTAAGWLLAHSTV (SEQ ID NO:232). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in epididymus, small intestine, and kidney.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, reproductive, renal, or gastrointestinal disorders, particularly degenerative kidney disease, congenital digestive disorders, and male infertility.

Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the urinary, digestive and male reproductive systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. reproductive, urogenital, intestinal, endothelial, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, seminal fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:139 as residues: Ala-59 to Thr-68, Glu-72 to Ser-108, Glu-115 to Lys-126.

The tissue distribution in kidney indicates that this gene or gene product could be used in the treatment and/or detection of kidney diseases including renal failure, nephritis, renal tubular acidosis, proteinuria, pyuria, edema, pyelonephritis, hydronephritis, nephrotic syndrome, crush syndrome, glomerulonephritis, hematuria, renal colic and kidney stones, in addition to Wilms Tumor Disease, and congenital kidney abnormalities such as horseshoe kidney, polycystic kidney, and Falconi's syndrome. Alternatively, expression within the epididymus indicates that the protein product of this gene may be useful for the detection, treatment, and/or prevention of a variety of reproductive disorders, particularly male infertility. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:37 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 940 of SEQ ID NO:37, b is an integer of 15 to 954, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:37, and where the b is greater than or equal to a + 14.

35 FEATURES OF PROTEIN ENCODED BY GENE NO: 28

In specific embodiments, polypeptides of the invention comprise the following amino acid sequence:

NSARDSLNTAIQAWQQNKCPEVEELVFSHFVICNDTQETLRFQVDTDENILLA
 SLHSHQYSWRSHKSPQ LLHICIEGWGNWRWSEPFSDHAGTFIRTIQYRGR
 5 TASLIKVQQLNGVQKQIIICGRQIICSYLSQSIE LKVVQHYIGQDGQAVVREHFD
 CLTAKQKLPSYILENNELTELCVKAKGDEDWSRDVCLESKAPEYSIVIQVPSS
 NSSIYVWCTVLTLEPNSQVQORMIVFSPLFIMRSHLPDPIIHLEKRSLGLSETQII
 PGKGQEKPLQNIEPDLVHHLTFQA (SEQ ID NO:233), NKCPEVEELVFSHF
 VICNDTQETLRF (SEQ ID NO:234), HICIEGWGNWRWSEPFSDHAGTFI (SEQ
 10 ID NO:235), VVREHFDCLTAKQKLPSYILENNELTE (SEQ ID NO:236), EDWSRD
 VCLESKAPEYSIVIQVPSSNS (SEQ ID NO:237), and/or IIHLEKRSLGLSETQII
 PGKGQEKPLQ (SEQ ID NO:238). Polynucleotides encoding these polypeptides are
 also encompassed by the invention. The gene encoding the disclosed cDNA is believed
 to reside on chromosome 8. Accordingly, polynucleotides related to this invention are
 15 useful as a marker in linkage analysis for chromosome 8.

This gene is expressed primarily in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as
 reagents for differential identification of the tissue(s) or cell type(s) present in a
 biological sample and for diagnosis of diseases and conditions which include, but are
 20 not limited to, disorders of the immune system, particularly immunodeficiencies, such as
 AIDS. Similarly, polypeptides and antibodies directed to these polypeptides are useful
 in providing immunological probes for differential identification of the tissue(s) or cell
 type(s). For a number of disorders of the above tissues or cells, particularly of for those
 of the immune system, expression of this gene at significantly higher or lower levels
 25 may be routinely detected in certain tissues or cell types (e.g. immune, hematopoietic,
 and cancerous and wounded tissues) or bodily fluids (e.g. lymph, serum, plasma,
 urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an
 individual having such a disorder, relative to the standard gene expression level, i.e.,
 the expression level in healthy tissue or bodily fluid from an individual not having the
 30 disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID
 NO:140 as residues: Met-1 to Gly-8, Thr-33 to Cys-38, Arg-79 to Arg-89.

The tissue distribution in immune cells indicates that polynucleotides and
 polypeptides corresponding to this gene are useful for the diagnosis and treatment of a
 variety of immune system disorders. Expression of this gene product in neutrophils
 35 indicates a role in the regulation of the proliferation; survival; differentiation; and/or
 activation of hematopoietic cell lineages, including blood stem cells. This gene product
 may be involved in the regulation of cytokine production, antigen presentation, or other

processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma,

5 immunodeficiency diseases such as AIDS, leukemia, rheumatoid arthritis, granulomatous disease, inflammatory bowel disease, sepsis, acne, neutropenia, neutrophilia, psoriasis, hypersensitivities, such as T-cell mediated cytotoxicity; immune reactions to transplanted organs and tissues, such as host-versus-graft and graft-versus-host diseases, or autoimmunity disorders, such as autoimmune infertility, lense tissue

10 injury, demyelination, systemic lupus erythematosus, drug induced hemolytic anemia, rheumatoid arthritis, Sjogren's disease, scleroderma and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show

15 utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:38 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the

20 scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 876 of SEQ ID NO:38, b is an integer of 15 to 890, where both a and b correspond to the positions of nucleotide residues shown in

25 SEQ ID NO:38, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 29

It has been discovered that the translation product of this gene shares homology

30 to a conserved *Caenorhabditis elegans* protein (See Genbank Accession No gil577546). In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: LIQDQTRRCHGLWHLPSLLWPLLWSSGTGLC RNVCRLHGIYHXVLXRVGHAYQTSFRQXVCXXWAADLCGRHEEGIIENTYRL SCNHVFHEFCIRGWCIVGKKQTCPYCKEKVDLKRMFSPWERPHVM

35 YGQLLDWLRYLVAWQPVTIGVVQGINYILG LE (SEQ ID NO:239), and/or TAFVTFRATRKLPLVQTTPRLVYKWFLLIYKISYATGIVGYMAVMFTLFGLNLLF KIKPEDAMDFGISLLFYGLYYGVLERDFAEMCADYMASTIXFXSESGMPT

KHLSDSXCAXCGQQIFVDVMKRGSLRTRIGCPAIMSSTSSASVAGASWER
SKRVPTAKRR (SEQ ID NO:240). Polynucleotides encoding these polypeptides are
also encompassed by the invention.

This gene is expressed primarily in embryonic brain.

5 Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions which include, but are
not limited to, neural disorders, particularly mental retardation of various types,
seizures, and mood disorders. Similarly, polypeptides and antibodies directed to these
10 polypeptides are useful in providing immunological probes for differential identification
of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells,
particularly of the central nervous system, expression of this gene at significantly higher
or lower levels may be routinely detected in certain tissues or cell types (e.g. neural,
developmental, and cancerous and wounded tissues) or bodily fluids (e.g. lymph,
15 amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue
or cell sample taken from an individual having such a disorder, relative to the standard
gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an
individual not having the disorder. Preferred epitopes include those comprising a
sequence shown in SEQ ID NO:141 as residues: Ser-22 to Met-28.

20 The tissue distribution in neural tissue indicates that polynucleotides and
polypeptides corresponding to this gene are useful for the detection/treatment of
neurodegenerative disease states, behavioural disorders, or inflammatory conditions such
as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome,
meningitis, encephalitis, demyelinating diseases, peripheral neuropathies, neoplasia,
25 trauma, congenital malformations, spinal cord injuries, ischemia and infarction,
aneurysms, hemorrhages, schizophrenia, mania, dementia, paranoia, obsessive
compulsive disorder, panic disorder, learning disabilities, ALS, psychoses, autism,
and altered behaviors, including disorders in feeding, sleep patterns, balance, and
preception. In addition, elevated expression of this gene product in regions of the brain
30 indicates that it plays a role in normal neural function. Potentially, this gene product is
involved in synapse formation, neurotransmission, learning, cognition, homeostasis, or
neuronal differentiation or survival. Moreover, the gene or gene product may also play a
role in the treatment and/or detection of developmental disorders associated with the
developing embryo, sexually-linked disorders, or disorders of the cardiovascular
35 system. Alternatively, expression within embryonic tissue indicates that this protein
may play a role in the regulation of cellular division, and may show utility in the
diagnosis and treatment of cancer and other proliferative disorders. Similarly,

developmental tissues rely on decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:39 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1056 of SEQ ID NO:39, b is an integer of 15 to 1070, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:39, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 30

It is likely that the sequence of this polynucleotide continues upstream of the preferred signal peptide. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence:
ATSMKRLSHPSICRTGLPLSQQKRASLL (SEQ ID NO:241). Polynucleotides encoding these polypeptides are also encompassed by the invention. When tested against Jurket cell lines, supernatants removed from cells containing this gene activated NF-kB (Nuclear Factor kB). Thus, it is likely that this gene activates immune cells through various signal transduction pathways. NF-kB is a transcription factor activated by a wide variety of agents, leading to cell activation, differentiation, or apoptosis. Reporter constructs utilizing the NF-kB promoter element are used to screen supernatants for such activity.

This gene is expressed primarily in early stage human embryos.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, developmental disorders, particularly various types of birth defects and congenital conditions. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells,

particularly for those of the developing embryo, expression of this gene at significantly higher or lower levels may be routinely detected in certain developing and, ultimately, adult, tissues or cell types (e.g. developmental, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution within embryonic tissue combined with the detected NF- κ B biological activity indicates that this protein may play a role in the regulation of cellular division, and may show utility in the diagnosis and treatment of cancer and other proliferative disorders. Similarly, developmental tissues rely on decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:40 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 758 of SEQ ID NO:40, b is an integer of 15 to 772, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:40, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 31

This gene is expressed primarily in breast.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of breast cancer and related disorders and disease. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the breast lymphatic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. breast, reproductive,

endocrine, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, breast milk, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:143 as residues: Lys-27 to Arg-41.

The tissue distribution in breast tissue indicates that the protein product of this gene may be useful for the detection, treatment, and/or prevention of disorders of the breast or reproductive tissue, particularly cancer. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:41 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 773 of SEQ ID NO:41, b is an integer of 15 to 787, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:41, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 32

This gene is expressed primarily in osteosarcoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of various skeletal disorders, particularly of osteosarcoma and related disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the skeletal and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.immune, skeletal, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an

individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:144 as residues: Trp-25 to Pro-33, Gln-88 to Pro-93.

The tissue distribution in skeletal tissue indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of a variety of skeletal disorders, such as osteosarcoma. Similarly, the expression of this gene product in osteo tissue would suggest a role in the detection and treatment of disorders and conditions affecting the skeletal system, in particular osteoporosis, bone cancer, as well as, disorders afflicting connective tissues (e.g. arthritis, trauma, tendonitis, chondromalacia and inflammation), such as in the diagnosis or treatment of various autoimmune disorders such as rheumatoid arthritis, lupus, scleroderma, and dermatomyositis as well as dwarfism, spinal deformation, and specific joint abnormalities as well as chondrodysplasias (ie. spondyloepiphyseal dysplasia congenita, familial osteoarthritis, Atelosteogenesis type II, metaphyseal chondrodysplasia type Schmid). Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:42 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 638 of SEQ ID NO:42, b is an integer of 15 to 652, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:42, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 33

The gene encoding the disclosed cDNA is believed to reside on chromosome 10. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 10.

This gene is expressed primarily in microvascular endothelial cells and in fetal liver cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cardiovascular, hematopoietic, immunological, or developmental

disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoietic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. cardiovascular, hematopoietic, immune, developmental, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in fetal liver indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of hematopoietic related disorders such as anemia, pancytopenia, leukopenia, thrombocytopenia or leukemia since stromal cells are important in the production of cells of hematopoietic lineages. The uses include bone marrow cell ex vivo culture, bone marrow transplantation, bone marrow reconstitution, radiotherapy or chemotherapy of neoplasia. The gene product may also be involved in lymphopoiesis, therefore, it can be used in immune disorders such as infection, inflammation, allergy, immunodeficiency etc. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Alternatively, expression within vascular tissue indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment, diagnosis, and/or prevention of a variety of vascular disorders, particularly cardiovascular disease, atherosclerosis, microvascular disease, stroke, embolism, or aneurysm. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:43 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1506 of SEQ ID NO:43, b is an integer of 15 to 1520, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:43, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 34

When tested against PC12 cell lines, supernatants removed from cells containing this gene activated the EGR1 (early growth response gene 1) promoter element. Thus, it is likely that this gene activates sensory neuron cells through the EGR1 signal transduction pathway. EGR1 is a separate signal transduction pathway from Jak-STAT, genes containing the EGR1 promoter are induced in various tissues and cell types upon activation, leading the cells to undergo differentiation and proliferation.

10 This gene is expressed primarily in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, immune system disorders, particularly inflammatory disorders such as arthritis and related conditions. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:146 as residues: Pro-18 to Glu-25.

The tissue distribution in immune cells combined with the detected EGR1 biological activity indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in neutrophils indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immunodeficiency diseases such as AIDS, leukemia, rheumatoid arthritis,

granulomatous disease, inflammatory bowel disease, sepsis, acne, neutropenia, neutrophilia, psoriasis, hypersensitivities, such as T-cell mediated cytotoxicity; immune reactions to transplanted organs and tissues, such as host-versus-graft and graft-versus-host diseases, or autoimmunity disorders, such as autoimmune infertility, lense tissue injury, demyelination, systemic lupus erythematosus, drug induced hemolytic anemia, rheumatoid arthritis, Sjogren's disease, scleroderma and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:44 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 782 of SEQ ID NO:44, b is an integer of 15 to 796, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:44, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 35

This gene is expressed primarily in brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, neural disorders, particularly mental retardation, mood disorders, epilepsy, learning disorders, and dementia. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. neural, cancerous and wounded tissues) or bodily fluids (e.g. lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene

expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in neural tissue indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states, behavioural disorders, or inflammatory conditions such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, meningitis, encephalitis, demyelinating diseases, peripheral neuropathies, neoplasia, trauma, congenital malformations, spinal cord injuries, ischemia and infarction, aneurysms, hemorrhages, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses, autism, and altered behaviors, including disorders in feeding, sleep patterns, balance, and preception. In addition, elevated expression of this gene product in regions of the brain indicates that it plays a role in normal neural function. Potentially, this gene product is involved in synapse formation, neurotransmission, learning, cognition, homeostasis, or neuronal differentiation or survival. Moreover, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:45 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1364 of SEQ ID NO:45, b is an integer of 15 to 1378, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:45, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 36

This gene is expressed in stage B2 prostate cancer.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, reproductive disorders, particularly proliferative disorders of the prostate

including benign prostatic hypertrophy. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the glandular or reproductive systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. reproductive, prostate, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, seminal fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in proliferate tissues indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis, and/or treating prostate disease including prostate cancer, or other reproductive conditions such as male infertility. Similarly, expression within cellular sources marked by proliferating cells indicates that this protein may play a role in the regulation of cellular division, and may show utility in the diagnosis and treatment of cancer and other proliferative disorders. Similarly, developmental tissues rely on decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:46 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 583 of SEQ ID NO:46, b is an integer of 15 to 597, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:46, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 37

When tested against U937 cell lines, supernatants removed from cells containing this gene activated the GAS (gamma activating sequence) promoter element. Thus, it is likely that this gene activates myeloid cells through the Jak-STAT signal

transduction pathway. GAS is a promoter element found upstream of many genes which are involved in the Jak-STAT pathway. The Jak-STAT pathway is a large, signal transduction pathway involved in the differentiation and proliferation of cells.

Therefore, activation of the Jak-STAT pathway, reflected by the binding of the GAS element, can be used to indicate proteins involved in the proliferation and differentiation of cells. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence:

MIILSCCSLWIYDYLIHPVPSVGHRVCLCCLPESATGRISPLGEGPRKWHGLRR
SPEHISLGGLLLSSRLMAFCNLSRAVLPGNRTMETETYQLWASQYQRKWVSR
LSQVQCLRL (SEQ ID NO:242). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in colorectal tumors.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancers of the colon, rectum or gastrointestinal tract. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the digestive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. gastrointestinal, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, bile, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:149 as residues: Phe-48 to Cys-54.

The tissue distribution in colorectal tumors indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment or diagnosis of tumors of the gastrointestinal tract, particularly of the colon or rectum. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:47 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence

described by the general formula of a-b, where a is any integer between 1 to 586 of SEQ ID NO:47, b is an integer of 15 to 600, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:47, and where the b is greater than or equal to a + 14.

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FEATURES OF PROTEIN ENCODED BY GENE NO: 38

It is likely that the sequence of this polynucleotide continues upstream of the preferred signal peptide. In specific embodiments, polypeptides of the invention
 10 comprise the following amino acid sequence:
 WIPRAAGIRHEHLSTLDRSVIWSKILNARCKICRKKGDAENMVLCDGC
 DRGHHTYCVRPKLKTVPEDWFCPECRPKQRSRLSSRQRPSLESDDEDVEDSM
 GGEDDEVGDGDEEEGQSE EEEYEVEQXEDDSXEEXEVRXVLXCNKMSQ (SEQ
 ID NO:243) and/orMRVARYVERKA (SEQ ID NO:244). Polynucleotides encoding
 15 these polypeptides are also encompassed by the invention.

This gene is expressed primarily in serum treated smooth muscle.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are
 20 not limited to, neuromuscular or vascular diseases, such as restenosis stroke, aneurysm, or atherosclerosis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the muscular and vascular systems, expression of this gene at significantly
 25 higher or lower levels may be routinely detected in certain tissues or cell types (e.g. vascular tissue, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an
 30 individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:150 as residues: Ser-46 to Trp-54, Lys-76 to Arg-86.

The tissue distribution in smooth muscle indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating restenosis or muscular responses due to degenerative conditions or injury. Protein, as well as, antibodies
 35 directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of

these sequences are related to SEQ ID NO:48 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention

5 are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 897 of SEQ ID NO:48, b is an integer of 15 to 911, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:48, and where the b is greater than or equal to a + 14.

10 FEATURES OF PROTEIN ENCODED BY GENE NO: 39

When tested against dermal fibroblast cell lines, supernatants removed from cells containing this gene activated the EGR1 (early growth response gene 1) promoter element. Thus, it is likely that this gene activates fibroblast cells through the EGR1

15 signal transduction pathway. EGR1 is a separate signal transduction pathway from Jak-STAT, genes containing the EGR1 promoter are induced in various tissues and cell types upon activation, leading the cells to undergo differentiation and proliferation. The gene encoding the disclosed cDNA is believed to reside on chromosome 3. Accordingly, polynucleotides related to this invention are useful as a marker in linkage

20 analysis for chromosome 3.

This gene is expressed in primary dendritic cells, and to a lesser extent, in human amygdala.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for diagnosis of diseases and conditions which include, but are not limited to,

25 immune or neural disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful to detect a number of disorders of the above tissues or cells, particularly of the vascular or neural system. Expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. immune, hematopoietic, neural, and cancerous and wounded tissues) or bodily

30 fluids (e.g. lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:151 as residues: Glu-30 to Gln-42.

35 The tissue distribution in primary dendritic cells indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of hematopoietic related disorders such as anemia, pancytopenia, leukopenia,

thrombocytopenia or leukemia since stromal cells are important in the production of cells of hematopoietic lineages. The uses include bone marrow cell ex vivo culture, bone marrow transplantation, bone marrow reconstitution, radiotherapy or chemotherapy of neoplasia. The gene product may also be involved in lymphopoiesis, therefore, it can be used in immune disorders such as infection, inflammation, allergy, immunodeficiency etc. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Alternatively, expression within the human amygdala indicates the the protein product of this gene may be useful for the treatment and/or diagnosis of a variety of neural disorders, particularly those involving processing of sensory information, including endocrine disorders as they relate to neural dysfunction. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. . Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:49 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1849 of SEQ ID NO:49, b is an integer of 15 to 1863, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:49, and where the b is greater than or equal to a + 14.

25 FEATURES OF PROTEIN ENCODED BY GENE NO: 40

The translation product of this gene shares sequence homology with the human rtvp-1 and glioma pathogenesis protein which are both glioma- specific proteins thought to be important in regulating the activity of extracellular proteases (See Genbank Accession No.gil1030053 and gil847722, respectively).In specific embodiments, polypeptides of the invention comprise the following amino acid sequence:
 QRWLKHGANQCKFEHNDCLDKSYKCYAAXEXVGENIWLGGIKSFTPRHAITA
 WYNETQFYDFDSLSCSRV CGHYTQLVWANSFYVGXAXAMCPNLGGASTAI
 FVCNYGPAGNFANMPYVVRGESCSLCSKEEKCCKNLCKNPFLKPTGRAPQQ
 TAFNPXQLRFSSSENLLMSFIYKRNSQMLK (SEQ ID NO:245). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in testes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, reproductive disorders, particular those disorders where proteases are thought to regulate the levels of secreted proteins including growth factors. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. reproductive, testes, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, seminal fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:152 as residues: Glu-43 to Asn-49.

The tissue distribution in testes combined with the homology to two conserved glioma-specific proteins indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating diseases of the reproductive system or diseases associated with increased degradation of secreted proteins or growth factors. The secreted protein can also be used to determine biological activity, to raise antibodies, as tissue markers, to isolate cognate ligands or receptors, to identify agents that modulate their interactions and as nutritional supplements. It may also have a very wide range of biological activities. Typical of these are cytokine, cell proliferation/differentiation modulating activity or induction of other cytokines; immunostimulating/immunosuppressant activities (e.g. for treating human immunodeficiency virus infection, cancer, autoimmune diseases and allergy); regulation of hematopoiesis (e.g. for treating anaemia or as adjunct to chemotherapy); stimulation or growth of bone, cartilage, tendons, ligaments and/or nerves (e.g. for treating wounds, stimulation of follicle stimulating hormone (for control of fertility); chemotactic and chemokinetic activities (e.g. for treating infections, tumors); hemostatic or thrombolytic activity (e.g. for treating haemophilia, cardiac infarction etc.); anti-inflammatory activity (e.g. for treating septic shock, Crohn's disease); as antimicrobials; for treating psoriasis or other hyperproliferative diseases; for regulation of metabolism, and behaviour. Also contemplated is the use of the corresponding nucleic acid in gene therapy procedures. Protein, as well as, antibodies directed against

the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:50 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 796 of SEQ ID NO:50, b is an integer of 15 to 810, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:50, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 41

It is likely that the sequence of this polynucleotide continues upstream of the preferred signal peptide. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence:
TEGGCALVPNDMESLKQKLVRVLEENLILSEKIQQLEEGAAISIVSGQQSHTYD
DLLHKNQQLTMQVACLNQELAQLKKLEKTVAILHESQRSLVVTNEYLL
QQLNKEPKGYSGKALLPPEKGHHLGRSSPFGKSTLSSSPVAHETGQYLIQSV
LDAAPEPGL (SEQ ID NO:246) and/or SMVSK (SEQ ID NO:247). Polynucleotides encoding these polypeptides are also encompassed by the invention. The gene encoding the disclosed cDNA is believed to reside on chromosome 16. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 16.

This gene is expressed primarily in lung and testes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, pulmonary or reproductive diseases such as adult respiratory distress syndrome (ARDS), pulmonary fibrositis or cystic fibrosis, or male infertility. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the respiratory system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. reproductive, pulmonary, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, pulmonary surfactant or

sputum, seminal fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:153 as residues: Ser-36 to Trp-41, Pro-53 to Arg-58.

The tissue distribution in lung tissue indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating disorders of the lung such as pulmonary fibrosis, cystic fibrosis or acute respiratory distress syndrome. Alternatively, the protein product of this gene may also be useful for the treatment and/or diagnosis of a variety of reproductive disorders, particularly male infertility or impotence, including disorders associated with testosterone regulation and secretion. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:51 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 942 of SEQ ID NO:51, b is an integer of 15 to 956, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:51, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 42

The translation product of this gene shares sequence homology with metallothioneins which are thought to be important in binding zinc and protecting cells from degeneration.

This gene is expressed primarily in the thyroid.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, endocrine disorders, particularly hypothyroidism. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a

number of disorders of the above tissues or cells, particularly of the endocrine system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. endocrine, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, serum, plasma, urine, synovial fluid and spinal fluid) or
 5 another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in endocrine tissue combined with the homology to metallothioneins indicates that polynucleotides and polypeptides corresponding to this
 10 gene are useful for treating disorders of the thyroid gland. Protein, as well as, antibodies directed against the protein may show utility as a tissue-specific marker and/or immunotherapy target for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:52 and may have been
 15 publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 286 of
 20 SEQ ID NO:52, b is an integer of 15 to 300, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:52, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 43

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It is likely that the sequence of this polynucleotide continues upstream of the preferred signal peptide. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence:

NTDWDQTVLIVLRISSTLPVALLRDEVPGWFLKXPEPQLISKELIMLTEV (SEQ
 30 ID NO:248). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in retinoic acid treated HL60 cells

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
 35 biological sample and for diagnosis of diseases and conditions which include, but are not limited to, immune disorders, particularly in the modulation of the immune response to infectious agents, or for acute or chronic inflammatory responses. Similarly,

polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For example, in a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:155 as residues: Pro-42 to Ser-50, Leu-52 to Phe-58, Pro-61 to Gly-73, Pro-76 to Gln-84.

The tissue distribution in HL60 cells indicates that polynucleotides and polypeptides corresponding to this gene are useful for modulating the immune response to an acute or chronic inflammation or to an infection. The secreted protein can also be used to determine biological activity, to raise antibodies, as tissue markers, to isolate cognate ligands or receptors, to identify agents that modulate their interactions and as nutritional supplements. It may also have a very wide range of biological activities. Typical of these are cytokine, cell proliferation/differentiation modulating activity or induction of other cytokines; immunostimulating/immunosuppressant activities (e.g. for treating human immunodeficiency virus infection, cancer, autoimmune diseases and allergy); regulation of hematopoiesis (e.g. for treating anaemia or as adjunct to chemotherapy); stimulation or growth of bone, cartilage, tendons, ligaments and/or nerves (e.g. for treating wounds, stimulation of follicle stimulating hormone (for control of fertility); chemotactic and chemokinetic activities (e.g. for treating infections, tumors); hemostatic or thrombolytic activity (e.g. for treating haemophilia, cardiac infarction etc.); anti-inflammatory activity (e.g. for treating septic shock, Crohn's disease); as antimicrobials; for treating psoriasis or other hyperproliferative diseases; for regulation of metabolism, and behaviour. Also contemplated is the use of the corresponding nucleic acid in gene therapy procedures. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:53 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention

are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 827 of SEQ ID NO:53, b is an integer of 15 to 841, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:53, and where the b is greater than or equal to a + 14.

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FEATURES OF PROTEIN ENCODED BY GENE NO: 44

This gene is expressed primarily in B-cell lymphoma .

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, immune disorders, such as proliferative compositions of the blood. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:156 as residues: Pro-38 to Asp-47, Ser-64 to Asn-71.

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The tissue distribution in immune tissue indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosing and treating tumors of the blood including B-Cell lymphomas. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immunodeficiency diseases such as AIDS, leukemia, rheumatoid arthritis, granulomatous disease, inflammatory bowel disease, sepsis, acne, neutropenia, neutrophilia, psoriasis, hypersensitivities, such as T-cell mediated cytotoxicity; immune reactions to transplanted organs and tissues, such as host-versus-graft and graft-versus-host diseases, or autoimmunity disorders, such as autoimmune infertility, lense tissue injury, demyelination, systemic lupus erythematosus, drug induced hemolytic anemia,

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rheumatoid arthritis, Sjogren's disease, scleroderma and tissues. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:54 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 620 of SEQ ID NO:54, b is an integer of 15 to 634, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:54, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 45

This gene is expressed primarily in cerebellum, and to a lesser extent, in other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of neuronal disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the cerebellum, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. brain, cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:157 as residues: Cys-56 to Ser-63, Met-67 to Leu-73.

The tissue distribution in neural tissue indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of neuronal disorders. The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of

neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses , autism, and altered bahaviors, including disorders in
5 feeding, sleep patterns, balance, and preception. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:55 and may have been publicly available prior to
10 conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 849 of SEQ ID NO:55, b is
15 an integer of 15 to 863, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:55, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 46

20 The gene encoding the disclosed cDNA is thought to reside on chromosome 14. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 14.

This gene is expressed primarily in colon, and to a lesser extent, in other tissues.

25 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of gastrointestinal disorders, particularly colon diseases, such as colon cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification
30 of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the colon, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder,
35 relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:158 as residues: Pro-26 to Asn-32.

The tissue distribution in colon tissues indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of colon-related diseases. Protein, as well as, antibodies directed against the protein may show utility as a tissue-specific marker and/or immunotherapy target for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:56 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 698 of SEQ ID NO:56, b is an integer of 15 to 712, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:56, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 47

This gene is expressed primarily in number of tumor tissues such as chondrosarcoma, synovial sarcoma, and to a lesser extent, in activated monocytes and T cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of tumorigenesis and hemapoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly tumors and other proliferate tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., skeletal, chondrocytes, fibroid, and cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in proliferative tissues indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of cell growth related disorders such as tumorigenesis and hemapoietic diseases. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker

and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:57 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 911 of SEQ ID NO:57, b is an integer of 15 to 925, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:57, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 48

This gene is expressed primarily in breast tissue and to a lesser extent in other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of breast diseases such as breast cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the breast, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. breast, cancerous and wounded tissues) or bodily fluids (e.g., lymph, breast milk, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in breast tissue indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of breast disorders such as breast cancer. Protein, as well as, antibodies directed against the protein may show utility as a tissue-specific marker and/or immunotherapy target for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:58 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is

cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 587 of SEQ ID NO:58, b is an integer of 15 to 601, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:58, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 49

When tested against Jurkat T-cell lines, supernatants removed from cells containing this gene activated the NF-kB assay. Thus, it is likely that this gene initiates cellular activation, differentiation, or apoptosis, as demonstrated by the NF-kB assay results. NF-kB (Nuclear factor kB) is a transcription factor activated by a wide variety of agents, leading to cell activation, differentiation, or apoptosis. Reporter constructs utilizing the NF-kB promoter element are used to screen supernatants for such activity. This gene is expressed primarily in chondrosarcoma, and to a lesser extent, in other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of chondrosarcoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly chondrosarcoma, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., chondrocytes, fibroid, cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of chondrosarcoma. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:59 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably

excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 716 of SEQ ID NO:59, b is an integer of 15 to 730, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:59, and where
5 the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 50

10 This gene is expressed primarily in human embryo and to a lesser extent in other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, embryonic or development disorders. Similarly, polypeptides and
15 antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the embryo, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. embryonic, cancerous and wounded tissues) or bodily fluids (e.g., lymph,
20 amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in developing tissue indicates that polynucleotides and
25 polypeptides corresponding to this gene are useful for diagnosis and treatment of embryonic development disorders. Embryonic development also involves decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could be useful in cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as
30 a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:60 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the
35 present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is

any integer between 1 to 832 of SEQ ID NO:60, b is an integer of 15 to 846, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:60, and where the b is greater than or equal to a + 14.

5 FEATURES OF PROTEIN ENCODED BY GENE NO: 51

The gene encoding the disclosed cDNA is thought to reside on chromosome 9. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 9.

- 10 This gene is expressed primarily in neuronal tissues, fetal tissues, and a number of cancer tissues and to a lesser extent in some other tissues.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, neuronal or early developmental disorders, and tumorigenesis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of neuronal tissues, fetal tissues, and some cancer tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. fetal tissues, brain, cancerous and wounded tissues) or bodily fluids (e.g., lymph, amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:163 as residues: Met-1 to Ser-6, Gln-59 to Gly-67.
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- The tissue distribution in neural and fetal tissues indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of neuronal disorders, early developmental disorders, and tumorigenesis. Embryonic development also involves decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:61 and may have been publicly available prior to conception of the present invention. Preferably, such related
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polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 944 of
5 SEQ ID NO:61, b is an integer of 15 to 958, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:61, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 52

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This gene is expressed primarily in fetal brain and to a lesser extent in other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
15 biological sample and for diagnosis of neuronal development disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the fetal brain, expression of this gene at significantly higher or lower levels may be routinely detected
20 in certain tissues or cell types (e.g. brain, cancerous and wounded tissues) or bodily fluids (e.g., lymph, amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include
25 those comprising a sequence shown in SEQ ID NO:164 as residues: Ser-25 to Tyr-35.

The tissue distribution in fetal brain indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of neuronal development disorders, fetal deficiencies, and pre-natal disorders. Expression within embryonic tissue and other cellular sources marked by proliferating cells
30 indicates that this protein may play a role in the regulation of cellular division, and may show utility in the diagnosis and treatment of cancer and other proliferative disorders. Similarly, embryonic development also involves decisions involving cell differentiation and/or apoptosis in pattern formation. Thus this protein may also be involved in apoptosis or tissue differentiation and could again be useful in cancer therapy. Protein,
35 as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through

sequence databases. Some of these sequences are related to SEQ ID NO:62 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably
5 excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 568 of SEQ ID NO:62, b is an integer of 15 to 582, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:62, and where the b is greater than or equal to a + 14.

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FEATURES OF PROTEIN ENCODED BY GENE NO: 53

When tested against both U937 myeloid and Jurkat T-cell cell lines, supernatants removed from cells containing this gene activated the GAS assay. Thus, it
15 is likely that this gene activates both myeloid cells and T-cells through the Jak-STAT signal transduction pathway. GAS (gamma activating sequence) is a promoter element found upstream of many genes which are involved in the Jak-STAT pathway. The Jak-STAT pathway is a large, signal transduction pathway involved in the differentiation and proliferation of cells. Therefore, activation of the Jak-STAT pathway, reflected by
20 the binding of the GAS element, can be used to indicate proteins involved in the proliferation and differentiation of cells.

This gene is expressed primarily in brain frontal cortex.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
25 biological sample and for diagnosis of neurological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected
30 in certain tissues or cell types (e.g. brain, cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those
35 comprising a sequence shown in SEQ ID NO:165 as residues: Gly-36 to Arg-43, Glu-50 to Glu-58.

The tissue distribution in frontal cortex indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses, autism, and altered bahaviors, including disorders in feeding, sleep patterns, balance, and perception. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:63 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 738 of SEQ ID NO:63, b is an integer of 15 to 752, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:63, and where the b is greater than or equal to a + 14.

20 FEATURES OF PROTEIN ENCODED BY GENE NO: 54

This gene is expressed primarily in the endometrium, and to a lesser extent, in other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of reproductive disorders and endometrial diseases such as endometrial tumors. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the endometrium, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. reproductive, cancerous and wounded tissues) or bodily fluids (e.g., lymph, amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:166 as residues: Arg-7 to Ser-14, Pro-32 to Leu-39.

The tissue distribution in endometrium indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of reproductive disorders, particularly endometrial diseases such as tumors or cancers of the endometrium. Given the tissue distribution, the protein product of this gene may also be useful in the treatment of reproductive disorders. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:64 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 692 of SEQ ID NO:64, b is an integer of 15 to 706, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:64, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 55

This gene is expressed primarily in activated T cells, and to a lesser extent, in other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of activated T-cells, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. immune, cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:167 as residues: Arg-35 to Gly-44.

The tissue distribution in T-cells indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of immune disorders. This gene product may be involved in the regulation of cytokine production, antigen

presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including

5 arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show

10 utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:65 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the

15 scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 386 of SEQ ID NO:65, b is an integer of 15 to 400, where both a and b correspond to the positions of nucleotide residues shown in

20 SEQ ID NO:65, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 56

This gene is expressed primarily in skin.

25 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions relating to skin. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell

30 type(s). For a number of disorders of the above tissues or cells, particularly of the endocrine system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. skin, cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder,

35 relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in integumentary tissue indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment, diagnosis, and/or prevention of various skin disorders including congenital disorders (i.e. nevi, moles, freckles, Mongolian spots, hemangiomas, port-wine syndrome), integumentary tumors (i.e. keratoses, Bowen's disease, basal cell carcinoma, squamous cell carcinoma, malignant melanoma, Paget's disease, mycosis fungoides, and Kaposi's sarcoma), injuries and inflammation of the skin (i.e. wounds, rashes, prickly heat disorder, psoriasis, dermatitis), atherosclerosis, urticaria, eczema, photosensitivity, autoimmune disorders (i.e. lupus erythematosus, vitiligo, dermatomyositis, morphea, scleroderma, pemphigoid, and pemphigus), keloids, striae, erythema, petechiae, purpura, and xanthelasma. Moreover, such disorders may predispose increased susceptibility to viral and bacterial infections of the skin (i.e. cold sores, warts, chickenpox, molluscum contagiosum, herpes zoster, boils, cellulitis, erysipelas, impetigo, tinea, athlete's foot, and ringworm). Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:66 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 759 of SEQ ID NO:66, b is an integer of 15 to 773, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:66, and where the b is greater than or equal to a + 14.

25 FEATURES OF PROTEIN ENCODED BY GENE NO: 57

This gene is expressed primarily in human fetal kidney.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of renal disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the urinary system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. developmental, renal, cancerous and wounded tissues) or bodily fluids (e.g., lymph, amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to

the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in fetal kidney indicates that this gene or gene product could be used in the treatment and/or detection of kidney diseases including renal failure, nephritis, renal tubular acidosis, proteinuria, pyuria, edema, pyelonephritis, hydronephritis, nephrotic syndrome, crush syndrome, glomerulonephritis, hematuria, renal colic and kidney stones, in addition to Wilms Tumor Disease, and congenital kidney abnormalities such as horseshoe kidney, polycystic kidney, and Falconi's syndrome. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:67 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 633 of SEQ ID NO:67, b is an integer of 15 to 647, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:67, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 58

This gene is expressed primarily in human fetal dura mater.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of disorders related to central nervous system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. brain, cancerous and wounded tissues) or bodily fluids (e.g., lymph, amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in dura mater indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and/or treatment of disorders of the brain and nervous system. Elevated expression of this gene product within the dura mater indicates that it may be involved in neuronal survival; synapse
5 formation; conductance; neural differentiation, etc. Such involvement may impact many processes, such as learning and cognition. It may also be useful in the treatment of such neurodegenerative disorders as schizophrenia; ALS; or Alzheimer's. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:68 and
10 may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is
15 any integer between 1 to 661 of SEQ ID NO:68, b is an integer of 15 to 675, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:68, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 59

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The translation product of this gene shares sequence homology with human beta-galactosidase (GLB1) mRNA. The gene encoding the disclosed cDNA is thought to reside on chromosome 3. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 3.

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This gene is expressed primarily in activated human neutrophil, and to a lesser extent in breast, kidney and gallbladder tissue.

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Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, immune, renal, metabolic or reproductive disorders, such as neutropenia and neutrophilia. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the disorders relating to hemopoietic system, expression of this gene at
35 significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. immune, cancerous and wounded tissues) or bodily fluids (e.g., lymph, bile, breast milk, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue

or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in neutrophils indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of immune disorders. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:69 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 875 of SEQ ID NO:69, b is an integer of 15 to 889, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:69, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 60

This gene is expressed primarily in human fetal kidney.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of renal disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the urinary system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell

types (e.g. renal, developmental, cancerous and wounded tissues) or bodily fluids (e.g., lymph, amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:172 as residues: Arg-27 to Asn-38, His-41 to Ser-54.

The tissue distribution in fetal kidney indicates that this gene or gene product could be used in the treatment and/or detection of kidney diseases including renal failure, nephritis, renal tubular acidosis, proteinuria, pyuria, edema, pyelonephritis, hydronephritis, nephrotic syndrome, crush syndrome, glomerulonephritis, hematuria, renal colic and kidney stones, in addition to Wilms Tumor Disease, and congenital kidney abnormalities such as horseshoe kidney, polycystic kidney, and Falconi's syndrome. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:70 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 874 of SEQ ID NO:70, b is an integer of 15 to 888, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:70, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 61

This gene is expressed primarily in human frontal cortex of an epileptic person. Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of epilepsy. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the PNS and CNS, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. brain, cancerous and wounded tissues) or bodily fluids (e.g., lymph,

serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

5 The tissue distribution in frontal cortex indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of epilepsy. Furthermore, the tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and/or treatment of disorders of the brain and nervous system. Elevated expression of this gene product
10 within the frontal cortex of the brain indicates that it may be involved in neuronal survival; synapse formation; conductance; neural differentiation, etc. Such involvement may impact many processes, such as learning and cognition. It may also be useful in the treatment of such neurodegenerative disorders as schizophrenia; ALS; or Alzheimer's. Many polynucleotide sequences, such as EST sequences, are publicly
15 available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:71 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more
20 polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 782 of SEQ ID NO:71, b is an integer of 15 to 796, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:71, and where the b is greater than or equal to a + 14.

25 **FEATURES OF PROTEIN ENCODED BY GENE NO: 62**

This gene is expressed primarily in human frontal cortex in a person with Schizophrenia.

Therefore, polynucleotides and polypeptides of the invention are useful as
30 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of neural conditions, particularly schizophrenic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of
35 the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. brain, cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial

fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:174 as residues:

5 Pro-49 to Gly-54.

The tissue distribution in frontal cortex indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and/or treatment of disorders of the brain and nervous system. Elevated expression of this gene product within the frontal cortex of the brain indicates that it may be involved in neuronal
10 survival; synapse formation; conductance; neural differentiation, etc. Such involvement may impact many processes, such as learning and cognition. It may also be useful in the treatment of such neurodegenerative disorders as schizophrenia; ALS; or Alzheimer's. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are
15 related to SEQ ID NO:72 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of
20 a-b, where a is any integer between 1 to 518 of SEQ ID NO:72, b is an integer of 15 to 532, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:72, and where the b is greater than or equal to a + 14.

25 FEATURES OF PROTEIN ENCODED BY GENE NO: 63

This gene is expressed primarily in hemangiopericytoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are
30 not limited to, benign disorders related to pericytes and endothelium-lined vessels. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nonmalignant character of neoplasm relating to pericytes and endothelial vessels,
35 expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. blood vessels, cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or

another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
5 corresponding to this gene are useful for diagnosis and treatment of
hemangiopericytoma. Protein, as well as, antibodies directed against the protein may
show utility as a tumor marker and/or immunotherapy targets for the above listed
tissues. Many polynucleotide sequences, such as EST sequences, are publicly available
and accessible through sequence databases. Some of these sequences are related to SEQ
10 ID NO:73 and may have been publicly available prior to conception of the present
invention. Preferably, such related polynucleotides are specifically excluded from the
scope of the present invention. To list every related sequence is cumbersome.
Accordingly, preferably excluded from the present invention are one or more
polynucleotides comprising a nucleotide sequence described by the general formula of
15 a-b, where a is any integer between 1 to 532 of SEQ ID NO:73, b is an integer of 15 to
546, where both a and b correspond to the positions of nucleotide residues shown in
SEQ ID NO:73, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 64

20

This gene is expressed primarily in hemangiopericytoma, and to a lesser extent
in human colon.

Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for differential identification of the tissue(s) or cell type(s) present in a
25 biological sample and for diagnosis of diseases and conditions which include, but are
not limited to, benign disorders related to pericytes and endothelium-lined vessels.
Similarly, polypeptides and antibodies directed to these polypeptides are useful in
providing immunological probes for differential identification of the tissue(s) or cell
type(s). For a number of disorders of the above tissues or cells, particularly of the
30 nonmalignant character of neoplasm relating to pericytes and endothelial vessels,
expression of this gene at significantly higher or lower levels may be routinely detected
in certain tissues or cell types (e.g. brain, cancerous and wounded tissues) or bodily
fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another
tissue or cell sample taken from an individual having such a disorder, relative to the
35 standard gene expression level, i.e., the expression level in healthy tissue or bodily
fluid from an individual not having the disorder. Preferred epitopes include those
comprising a sequence shown in SEQ ID NO:176 as residues: Lys-39 to Glu-45.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of hemangiopericytoma. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:74 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome.

Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 701 of SEQ ID NO:74, b is an integer of 15 to 715, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:74, and where the b is greater than or equal to a + 14.

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FEATURES OF PROTEIN ENCODED BY GENE NO: 65

This gene is expressed primarily in glioblastoma, and to a lesser extent in B-cell lymphoma and anergic T-cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, disorders related to neuroglial and ependymal cells, as well as the immune system, including tumors. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system or immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. brain, immune, cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in glioblastoma indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of neural cell disorders. Furthermore, the tissue distribution indicates that the translation product of this gene is useful for the treatment and/or detection of tumors of the brain and

immune system, such as glioblastomas and B-cell lymphomas. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:75 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 392 of SEQ ID NO:75, b is an integer of 15 to 406, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:75, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 66

This gene is expressed primarily in skin.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions relating to skin. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the endocrine system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. skin, cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:178 as residues: Pro-27 to Pro-40.

The tissue distribution in integumentary tissue indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment, diagnosis, and/or prevention of various skin disorders including congenital disorders (i.e. nevi, moles, freckles, Mongolian spots, hemangiomas, port-wine syndrome), integumentary tumors (i.e. keratoses, Bowen's disease, basal cell carcinoma, squamous cell carcinoma, malignant melanoma, Paget's disease, mycosis fungoides, and Kaposi's sarcoma), injuries and inflammation of the skin (i.e. wounds, rashes, prickly heat disorder, psoriasis, dermatitis), atherosclerosis, urticaria, eczema, photosensitivity, autoimmune disorders (i.e. lupus erythematosus, vitiligo, dermatomyositis, morphea, scleroderma,

pemphigoid, and pemphigus), keloids, striae, erythema, petechiae, purpura, and xanthelasma. Moreover, such disorders may predispose increased susceptibility to viral and bacterial infections of the skin (i.e. cold sores, warts, chickenpox, molluscum contagiosum, herpes zoster, boils, cellulitis, erysipelas, impetigo, tinea, athlete's foot, and ringworm). Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:76 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 528 of SEQ ID NO:76, b is an integer of 15 to 542, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:76, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 67

This gene is expressed primarily in brain frontal cortex.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, neurological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. brain, cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:179 as residues: Gly-27 to Pro-34, Tyr-59 to Arg-65.

The tissue distribution in frontal cortex indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and/or treatment of disorders of the brain and nervous system. Elevated expression of this gene product within the frontal cortex of the brain indicates that it may be involved in neuronal survival; synapse formation; conductance; neural differentiation, etc. Such involvement

may impact many processes, such as learning and cognition. It may also be useful in the treatment of such neurodegenerative disorders as schizophrenia; ALS; or Alzheimer's. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are
5 related to SEQ ID NO:77 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of
10 a-b, where a is any integer between 1 to 406 of SEQ ID NO:77, b is an integer of 15 to 420, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:77, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 68

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This gene is expressed primarily in human frontal cortex of a person exhibiting Schizophrenia.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
20 biological sample and for diagnosis of neural conditions, particularly Schizophrenic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower
25 levels may be routinely detected in certain tissues or cell types (e.g. brain, cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

30

The tissue distribution in frontal cortex indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and/or treatment of disorders of the brain and nervous system. Elevated expression of this gene product within the frontal cortex of the brain indicates that it may be involved in neuronal survival; synapse formation; conductance; neural differentiation, etc. Such involvement
35 may impact many processes, such as learning and cognition. It may also be useful in the treatment of such neurodegenerative disorders as schizophrenia; ALS; or Alzheimer's. Many polynucleotide sequences, such as EST sequences, are publicly

available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:78 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome.

- 5 Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 451 of SEQ ID NO:78, b is an integer of 15 to 465, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:78, and where the b is greater than or equal to a + 14.

10

FEATURES OF PROTEIN ENCODED BY GENE NO: 69

This gene is expressed primarily in glioblastoma.

- Therefore, polynucleotides and polypeptides of the invention are useful as
- 15 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, disorders related to neuroglial and ependymal cells, including cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell
- 20 type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. brain, cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a
- 25 disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- The tissue distribution in glioblastoma indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of neural cell disorders. Furthermore, given the tissue distribution, the translation product of this
- 30 gene may be useful for the intervention or detection of tumors of the brain, such as glioblastomas. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:79 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded
- 35 from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of

a-b, where a is any integer between 1 to 876 of SEQ ID NO:79, b is an integer of 15 to 890, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:79, and where the b is greater than or equal to a + 14.

5 FEATURES OF PROTEIN ENCODED BY GENE NO: 70

This gene is expressed primarily in human fetal brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, immune, growth, or neurologic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the CNS and immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. brain, immune, cancerous and wounded tissues) or bodily fluids (e.g., lymph, amniotic fluid, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:182 as residues: Lys-13 to Asn-19, Asn-27 to Asn-35.

The tissue distribution in fetal brain indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection and treatment of disorders of the central nervous system and immune system. The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses, autism, and altered behaviors, including disorders in feeding, sleep patterns, balance, and perception. In addition, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo or sexually-linked disorders. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:80 and

may have been publicly available prior to conception of the present invention.

Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides

- 5 comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 456 of SEQ ID NO:80, b is an integer of 15 to 470, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:80, and where the b is greater than or equal to a + 14.

10 FEATURES OF PROTEIN ENCODED BY GENE NO: 71

This gene is expressed primarily in human epithelioid sarcoma, and to a lesser extent in breast cancer and adrenal gland tumors.

- 15 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, disorders related to epithelium, and cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders
- 20 of the above tissues or cells, particularly of the endocrine system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., integumentary, fibroid, epithelial, reproductive, cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a
- 25 disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- The tissue distribution in epithelial sarcoma indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of epithelial disorders. Furthermore, the tissue distribution indicates that polynucleotides
- 30 and polypeptides corresponding to this gene are useful for the detection, treatment, and/or prevention of various endocrine disorders and cancers, particularly Addison's disease, Cushing's Syndrome, and disorders and/or cancers of the pancreas (e.g. diabetes mellitus), adrenal cortex, pituitary (e.g., hyper-, hypopituitarism), thyroid (e.g. hyper-, hypothyroidism), parathyroid (e.g. hyper-, hypoparathyroidism), and
- 35 hypothalamus. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available

and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:81 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome.

- 5 Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1076 of SEQ ID NO:81, b is an integer of 15 to 1090, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:81, and where the b is greater than or equal to a + 14.

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FEATURES OF PROTEIN ENCODED BY GENE NO: 72

When tested against U937 cell lines, supernatants removed from cells containing this gene activated the GAS (gamma activating sequence) promoter element.

- 15 Thus, it is likely that this gene activates myeloid cells through the Jak-STAT signal transduction pathway. GAS is a promoter element found upstream of many genes which are involved in the Jak-STAT pathway. The Jak-STAT pathway is a large, signal transduction pathway involved in the differentiation and proliferation of cells. Therefore, activation of the Jak-STAT pathway, reflected by the binding of the GAS
20 element, can be used to indicate proteins involved in the proliferation and differentiation of cells.

This gene is expressed primarily in brain-medulloblastoma.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
25 biological sample and for diagnosis of diseases and conditions which include, but are not limited to, neural disorders, particularly proliferative conditions such as brain-medulloblastoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells,
30 particularly of the nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. neural, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the
35 expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:184 as residues: Asp-18 to His-25, Phe-55 to Tyr-69.

The tissue distribution in brain-medulloblastoma indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and intervention of brain-medulloblastoma or other tumors. Additionally, the peptide may act in nerve tissue development and functions. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:82 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 684 of SEQ ID NO:82, b is an integer of 15 to 698, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:82, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 73

In specific embodiments, polypeptides of the invention comprise the following amino acid sequence:
VAESTEEPAGSNRGQYPEDSSSDGLRQREVLRLNLSSPGWENISR (SEQ ID NO:249). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in chronic lymphocytic leukemia.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, hemapoietic or immune disorders, particularly leukemic diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hemapoietic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the

expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in lymphocytic leukemia indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and intervention of leukemic diseases and hemapoietic disorders. Similarly, expression within hematopoietic cells indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of hematopoietic related disorders such as anemia, pancytopenia, leukopenia, thrombocytopenia or leukemia since stromal cells are important in the production of cells of hematopoietic lineages. The uses include bone marrow cell ex vivo culture, bone marrow transplantation, bone marrow reconstitution, radiotherapy or chemotherapy of neoplasia. The gene product may also be involved in lymphopoiesis, therefore, it can be used in immune disorders such as infection, inflammation, allergy, immunodeficiency etc. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:83 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 854 of SEQ ID NO:83, b is an integer of 15 to 868, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:83, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 74

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It is likely that the open reading frame containing the predicted signal peptide continues in the 5' direction. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence:

AREPLGLTQDPLVFGMTSFLQTSSPIPNSC (SEQ ID NO:250). Polynucleotides encoding these polypeptides are also encompassed by the invention. The gene encoding the disclosed cDNA is believed to reside on chromosome 11. Accordingly,

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polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 11.

This gene is expressed primarily in endothelial cells and in brain.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, hematopoietic and neurological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders
10 of the above tissues or cells, particularly of the vascular and nervous systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. immune, hematopoietic, neural, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a
15 disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:186 as residues: Ser-34 to Ser-39.

The tissue distribution in neural tissue indicates that polynucleotides and
20 polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states, behavioural disorders, or inflammatory conditions such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, meningitis, encephalitis, demyelinating diseases, peripheral neuropathies, neoplasia, trauma, congenital malformations, spinal cord injuries, ischemia and infarction,
25 aneurysms, hemorrhages, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses, autism, and altered behaviors, including disorders in feeding, sleep patterns, balance, and preception. In addition, elevated expression of this gene product in regions of the brain indicates that it plays a role in normal neural function. Potentially, this gene product is
30 involved in synapse formation, neurotransmission, learning, cognition, homeostasis, or neuronal differentiation or survival. Moreover, the gene or gene product may also play a role in the treatment and/or detection of developmental disorders associated with the developing embryo, sexually-linked disorders, or disorders of the cardiovascular system. Protein, as well as, antibodies directed against the protein may show utility as a
35 tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:84 and

may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 615 of SEQ ID NO:84, b is an integer of 15 to 629, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:84, and where the b is greater than or equal to a + 14.

10 FEATURES OF PROTEIN ENCODED BY GENE NO: 75

It is likely that the open reading frame containing the predicted signal peptide continues in the 5' direction. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: FQAPASARTACSTLL (SEQ ID NO:251). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, immune and hematopoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:187 as residues: Val-24 to Ser-29, Ser-53 to Ala-59, Glu-69 to Met-74.

The tissue distribution predominantly in neutrophils indicates that the gene could be important for the treatment or detection of immune or hematopoietic disorders including arthritis, asthma, immunodeficiency diseases, leukemia, transplant rejection, and microbial infections. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed

tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:85 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 823 of SEQ ID NO:85, b is an integer of 15 to 837, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:85, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 76

It is likely that the open reading frame containing the predicted signal peptide continues in the 5' direction. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence:
 AQPSPCPSCLAHSWPPFRLLSLPPAGASLGDRVCS (SEQ ID NO:252), and/or
 HSLPPALPAWLTPGHPSDSSLCLLQLAPHLVMAVSVPWPLPEXLGFSCCHCVS
 LTGPHAGFSYHFLHPAEPRAWQHQS SVVGMSRKQASFSMAQKGVCHLG
 KSXKRGSKKASCPXYPFSK (SEQ ID NO:253). Polynucleotides encoding these polypeptides are also encompassed by the invention.

This gene is expressed primarily in endothelial cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, integumentary or vascular disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoietic and vascular systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. cardiovascular, immune, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution of this gene in endothelial cells indicates that be useful in the treatment and detection of hematopoietic, immune and/or vascular disorders,

particularly atherosclerosis, embolism, stroke, or aneurysm. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:86 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 889 of SEQ ID NO:86, b is an integer of 15 to 903, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:86, and where the b is greater than or equal to a + 14.

15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 77**

This gene is expressed primarily in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, hematopoietic and immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoietic and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:189 as residues: Gly-33 to Asn-44.

The tissue distribution in neutrophils indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of hematopoietic and immune disorders including: anemias, auto-immunities, immunodeficiencies (e.g. AIDS), immuno-suppressive conditions (transplantation) and leukemias. In addition this gene product may be applicable in conditions of general microbial infection, arthritis, inflammation or cancer. Protein, as well as, antibodies

directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:87 and may have been publicly available
5 prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 711 of SEQ ID NO:87, b is
10 an integer of 15 to 725, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:87, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 78

15 This gene is expressed primarily in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, hematopoietic and immune disorders. Similarly, polypeptides and
20 antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoietic and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. immune, hematopoietic, and cancerous and wounded
25 tissues) or bodily fluids (e.g. lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in neutrophils indicates that polynucleotides and
30 polypeptides corresponding to this gene are useful for the diagnosis and treatment of hematopoietic and immune disorders including: anemias, auto-immunities, immunodeficiencies (e.g. AIDS), immuno-suppressive conditions (transplantation) and leukemias. In addition this gene product may be applicable in conditions of general microbial infection, arthritis, inflammation or cancer. Protein, as well as, antibodies
35 directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of

these sequences are related to SEQ ID NO:88 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention
5 are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 592 of SEQ ID NO:88, b is an integer of 15 to 606, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:88, and where the b is greater than or equal to a + 14.

10 FEATURES OF PROTEIN ENCODED BY GENE NO: 79

This gene is expressed primarily in hematopoietic cells including neutrophils, T-cells and activated monocytes.

Therefore, polynucleotides and polypeptides of the invention are useful as
15 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, hematopoietic and immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders
20 of the above tissues or cells, particularly of the hematopoietic and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. immune, hematopoietic, and cancerous and wounded tissues) or bodily fluids (e.g. lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder,
25 relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution of this gene predominantly in hematopoietic cell types indicates that the gene could be important for the treatment or detection of immune or hematopoietic disorders including arthritis, asthma, immunodeficiency diseases and
30 leukemia. Moreover, this gene would also be useful for the treatment and diagnosis of other hematopoietic related disorders such as anemia, pancytopenia, leukopenia, or thrombocytopenia since stromal cells are important in the production of cells of hematopoietic lineages. The uses include bone marrow cell ex vivo culture, bone marrow transplantation, bone marrow reconstitution, radiotherapy or chemotherapy of
35 neoplasia. The gene product may also be involved in lymphopoiesis, therefore, it can be used in immune disorders such as infection, inflammation, allergy, immunodeficiency etc. In addition, this gene product may have commercial utility in the expansion of stem

cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:89 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1128 of SEQ ID NO:89, b is an integer of 15 to 1142, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:89, and where the b is greater than or equal to a + 14.

15 FEATURES OF PROTEIN ENCODED BY GENE NO: 80

It is likely that the open reading frame containing the predicted signal peptide continues in the 5' direction. In specific embodiments, polypeptides of the invention comprise the following amino acid sequence: IGIRVWYYRNQKNSKQMWIKCLGS (SEQ ID NO:254). Polynucleotides encoding these polypeptides are also encompassed by the invention. The gene encoding the disclosed cDNA is believed to reside on chromosome 1. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 1.

This gene is expressed primarily in endothelial cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, integumentary or vascular disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the vascular and hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. vascular, integumentary, cancerous and wounded tissues) or bodily fluids (e.g. lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in vascular tissue indicates that the protein product of this gene may be useful in the treatment, and/or prevention of a variety of vascular conditions such as atherosclerosis, aneurysm, stroke, or embolism. As the gene is expressed in endothelial cells, it may also be of importance in the treatment and detection of hematopoietic, and/or immune disorders. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:90 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 582 of SEQ ID NO:90, b is an integer of 15 to 596, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:90, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 81

The translation product of this gene shares sequence homology with the bile acid CoA:amino acid N-acyltransferase (BAT) which is thought to be important as a liver enzyme that catalyzes the conjugation of bile acids with glycine or taurine (See Genbank Accession No.gnllPIDle307059).

This gene is expressed primarily in hepatocellular tumor.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, liver diseases and hepatocellular carcinoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hepatocellular carcinoma, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g.hepatic, and cancerous and wounded tissues) or bodily fluids (e.g.lymph, bile, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those

comprising a sequence shown in SEQ ID NO:193 as residues: Thr-55 to Gln-66, Asp-85 to Glu-92, Pro-125 to Ser-130, Gly-146 to Ala-154, Leu-170 to Lys-177.

The tissue distribution in hepatocellular tumor and homology to bile acid CoA:amino acid N-acyltransferase (BAT) indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and intervention of hepatocellular tumor, particularly as a new molecular prognostic marker in hepatocellular carcinoma patients, following hepatic resection. Moreover, the protein product of this gene would also be useful for the detection and treatment of other liver disorders and cancers (e.g. hepatoblastoma, jaundice, hepatitis, liver metabolic diseases and conditions that are attributable to the differentiation of hepatocyte progenitor cells). The protein may also be useful in developmental abnormalities, fetal deficiencies, pre-natal disorders and various wound-healing models and/or tissue trauma. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:91 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 619 of SEQ ID NO:91, b is an integer of 15 to 633, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:91, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 82

This gene is expressed primarily in bone marrow.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, hematopoietic and immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoietic and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. immune, bone, cancerous and wounded tissues) or

bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- 5 The tissue distribution of this gene in bone marrow indicates that the gene could be important for the treatment or detection of immune or hematopoietic disorders including arthritis, asthma, immunodeficiency diseases, leukemia, and also in treatment of cancer patients with a depleted immune system. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or
- 10 immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:92 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To
- 15 list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 711 of SEQ ID NO:92, b is an integer of 15 to 725, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:92, and where the b is greater
- 20 than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 83

- 25 When tested against K562 leukemia cell lines, supernatants removed from cells containing this gene activated the ISRE assay. Thus, it is likely that this gene activates leukemia cells through the Jak-STAT signal transduction pathway. The ISRE (interferon-sensitive responsive element) is a promoter element found upstream in many genes involved in the Jak-STAT pathway. The Jak-STAT pathway is a large, signal transduction pathway involved in the differentiation and proliferation of cells.
- 30 Therefore, activation of the Jak-STAT pathway, reflected by the binding of the ISRE element, can be used to indicate proteins involved in the proliferation and differentiation of cells.

 This gene is expressed primarily in neutrophils.

- 35 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, immunologically mediated disorders. Similarly, polypeptides and

antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected
5 in certain tissues or cell types (e.g. immune, cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

10 The tissue distribution in neutrophils indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of hematopoietic and immune disorders including: anemias, auto-immunities, immunodeficiencies (e.g. AIDS), immuno-suppressive conditions (transplantation) and leukemias. In addition this gene product may be applicable in conditions of general
15 microbial infection, inflammation or cancer. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:93 and may have been publicly available prior to
20 conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 587 of SEQ ID NO:93, b is
25 an integer of 15 to 601, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:93, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 84

30 This gene is expressed primarily in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, immune and hematopoietic disorders. Similarly, polypeptides and
35 antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and hematopoietic systems,

expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. immune, cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:196 as residues: Trp-22 to Trp-35, Ser-42 to Gly-50.

The tissue distribution of this gene predominantly in neutrophils indicates that the gene could be important for the treatment or detection of immune or hematopoietic disorders including arthritis, asthma, immunodeficiency diseases, leukemia, transplant rejection, and microbial infections. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:94 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 678 of SEQ ID NO:94, b is an integer of 15 to 692, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:94, and where the b is greater than or equal to a + 14.

25 FEATURES OF PROTEIN ENCODED BY GENE NO: 85

This gene is expressed primarily in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, immunological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. immune, cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another

tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:197 as residues: Asn-51 to Asn-69.

5 The tissue distribution in neutrophils indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of hematopoietic and immune disorders including: anemias, auto-immunities, immunodeficiencies (e.g. AIDS), immuno-suppressive conditions (transplantation) and leukemias. In addition this gene product may be applicable in conditions of general
10 microbial infection, inflammation or cancer. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:95 and may have been publicly available prior to
15 conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 991 of SEQ ID NO:95, b is
20 an integer of 15 to 1005, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:95, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 86

25 This gene is expressed primarily in brain medulloblastoma.

 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer, neurodegenerative diseases and behavioural disorders.
30 Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. brain, cancerous and wounded
35 tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder,

relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in brain tissue indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of
5 cancers of the brain, such as medulloblastomas. Furthermore, the tissue distribution also indicates that the translation product of this gene is useful for the detection and/or treatment of neurodegenerative disease states and behavioural disorders such as
Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, schizophrenia, mania,
dementia, paranoia, obsessive compulsive disorder and panic disorder. Protein, as well
10 as, antibodies directed against the protein may show utility as a tissue-specific marker and/or immunotherapy target for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:96 and may have been publicly available prior to conception of the present invention. Preferably,
15 such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 598 of SEQ ID NO:96, b is an integer of 15 to 612, where both a and b
20 correspond to the positions of nucleotide residues shown in SEQ ID NO:96, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 87

25 This gene is expressed primarily in brain, bone marrow, lung, and to a lesser extent, in other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are
30 not limited to, disorders of the brain and lungs. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, CNS, and pulmonary systems expression of this gene at significantly higher or lower levels may be routinely detected
35 in certain tissues or cell types (e.g. brain, lung, immune, cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder,

relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in bone marrow indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of hematopoietic related disorders such as anemia, pancytopenia, leukopenia, thrombocytopenia or leukemia since stromal cells are important in the production of cells of hematopoietic lineages. The uses include bone marrow cell ex vivo culture, bone marrow transplantation, bone marrow reconstitution, radiotherapy or chemotherapy of neoplasia. The gene product may also be involved in lymphopoiesis, therefore, it can be used in immune disorders such as infection, inflammation, allergy, immunodeficiency etc. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Furthermore, the tissue distribution in brain tissue indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection/treatment of neurodegenerative disease states and behavioural disorders such as Alzheimers Disease, Parkinsons Disease, Huntingtons Disease, Tourette Syndrome, schizophrenia, mania, dementia, paranoia, obsessive compulsive disorder, panic disorder, learning disabilities, ALS, psychoses, autism, and altered behaviors, including disorders in feeding, sleep patterns, balance, and perception. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:97 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 656 of SEQ ID NO:97, b is an integer of 15 to 670, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:97, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 88

This gene is expressed primarily in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a

biological sample and for diagnosis of diseases and conditions which include, but are not limited to, hematopoietic and immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders
5 of the above tissues or cells, particularly of the hematopoietic and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. immune, cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the
10 standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in neutrophils indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in immune cells
15 indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of
20 lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. In addition, this gene product may have commercial utility in the expansion of stem cells and committed
25 progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID
30 NO:98 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of
35 a-b, where a is any integer between 1 to 605 of SEQ ID NO:98, b is an integer of 15 to 619, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:98, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 89

This gene is expressed primarily in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions which include, but are
not limited to, hematopoietic and immune system disorders. Similarly, polypeptides
and antibodies directed to these polypeptides are useful in providing immunological
10 probes for differential identification of the tissue(s) or cell type(s). For a number of
disorders of the above tissues or cells, particularly of the hematopoietic and immune
systems, expression of this gene at significantly higher or lower levels may be routinely
detected in certain tissues or cell types (e.g. immune, cancerous and wounded tissues)
or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or
15 another tissue or cell sample taken from an individual having such a disorder, relative to
the standard gene expression level, i.e., the expression level in healthy tissue or bodily
fluid from an individual not having the disorder.

The tissue distribution in neutrophils indicates that polynucleotides and
polypeptides corresponding to this gene are useful for the diagnosis and treatment of a
variety of immune system disorders. Expression of this gene product in immune cells
20 indicates a role in the regulation of the proliferation; survival; differentiation; and/or
activation of potentially all hematopoietic cell lineages, including blood stem cells. This
gene product may be involved in the regulation of cytokine production, antigen
presentation, or other processes that may also suggest a usefulness in the treatment of
cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of
25 lymphoid origin, the natural gene product may be involved in immune functions.
Therefore it may be also used as an agent for immunological disorders including
arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid
arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. In addition, this gene
product may have commercial utility in the expansion of stem cells and committed
30 progenitors of various blood lineages, and in the differentiation and/or proliferation of
various cell types. Protein, as well as, antibodies directed against the protein may show
utility as a tumor marker and/or immunotherapy targets for the above listed tissues.
Many polynucleotide sequences, such as EST sequences, are publicly available and
accessible through sequence databases. Some of these sequences are related to SEQ ID
35 NO:99 and may have been publicly available prior to conception of the present
invention. Preferably, such related polynucleotides are specifically excluded from the
scope of the present invention. To list every related sequence is cumbersome.

Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 689 of SEQ ID NO:99, b is an integer of 15 to 703, where both a and b correspond to the positions of nucleotide residues shown in
5 SEQ ID NO:99, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 90

10 This gene is expressed primarily in neutrophils. It is likely that a frame shift exists in the sequence, and these are easily resolved by those skilled in the art using known molecular biology techniques.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are
15 not limited to, hematopoietic and immune system disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoietic and immune systems, expression of this gene at significantly higher or lower levels may be routinely
20 detected in certain tissues or cell types (e.g. immune, cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

25 The tissue distribution in neutrophils indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in immune cells indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This
30 gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including
35 arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. In addition, this gene product may have commercial utility in the expansion of stem cells and committed

progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:100 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 748 of SEQ ID NO:100, b is an integer of 15 to 762, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:100, and where the b is greater than or equal to a + 14.

15 FEATURES OF PROTEIN ENCODED BY GENE NO: 91

Contact of cells with supernatant containing the expressed product of this gene increases the permeability of the plasma membrane of astrocytes to calcium. Thus, it is likely that the product of this gene is involved in a signal transduction pathway that is initiated when the product binds a receptor on the surface of the astrocytes. Thus, polynucleotides and polypeptides of this gene have uses which include, but are not limited to, activating astrocytes.

This gene is expressed primarily in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, hematopoietic and immune system disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoietic and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. immune, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:203 as residues: Met-1 to Glu-6.

The tissue distribution in neutrophils indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of a variety of immune system disorders. Expression of this gene product in immune cells indicates a role in the regulation of the proliferation; survival; differentiation; and/or

5 activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions.

10 Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of

15 various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:101 and may have been publicly available prior to conception of the present

20 invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 636 of SEQ ID NO:101, b is an integer of 15

25 to 650, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:101, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 92

30 This gene is expressed primarily in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, hematopoietic and immune system disorders. Similarly, polypeptides

35 and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoietic and immune

systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. immune, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the
5 standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:204 as residues: Ile-4 to Cys-9, Ser-36 to Asp-49, Ile-107 to Ile-115.

The tissue distribution in neutrophils indicates that polynucleotides and
10 polypeptides corresponding to this gene are useful for the diagnosis and treatment of hematopoietic and immune system disorders including: anemias, auto-immunities, immunodeficiencies (e.g. AIDS), immuno-suppressive conditions (transplantation) and leukemias. In addition this gene product may be applicable in conditions of general microbial infection, arthritis, inflammation or cancer. Protein, as well as, antibodies
15 directed against the protein may show utility as a tissue-specific marker and/or immunotherapy target for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:102 and may have been publicly available prior to conception of the present invention. Preferably, such related
20 polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 346 of SEQ ID NO:102, b is an integer of 15 to 360, where both a and b correspond to the
25 positions of nucleotide residues shown in SEQ ID NO:102, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 93

30 This gene is expressed primarily in hemangiopericytoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, hemangiopericytoma. Similarly, polypeptides and antibodies directed to
35 these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the capillaries and arterioles, expression of this gene at

significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. circulatory, cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:205 as residues: Thr-46 to Asp-52.

The tissue distribution in hemangiopericytoma indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and intervention of hemangiopericytoma or other pericyte related diseases. Protein, as well as, antibodies directed against the protein may show utility as a tissue-specific marker and/or immunotherapy target for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:103 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 803 of SEQ ID NO:103, b is an integer of 15 to 817, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:103, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 94

This gene is expressed primarily in bone marrow.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, hematopoietic and immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoietic and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. immune, bone, cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to

the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution of this gene in bone marrow indicates that the gene could be important for the treatment or detection of immune or hematopoietic disorders including arthritis, asthma, immunodeficiency diseases, leukemia, and also in the treatment of cancer patients with a depleted immune system. The polypeptides or polynucleotides are also useful to enhance or protect proliferation, differentiation, and functional activation of hematopoietic progenitor cells (e.g., bone marrow cells), useful in treating cancer patients undergoing chemotherapy or patients undergoing bone marrow transplantation. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:104 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 867 of SEQ ID NO:104, b is an integer of 15 to 881, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:104, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 95

The gene encoding the disclosed cDNA is thought to reside on chromosome 4. Accordingly, polynucleotides related to this invention are useful as a marker in linkage analysis for chromosome 4.

This gene is expressed primarily in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, immune and hematopoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoietic and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. immune, cancerous and wounded tissues) or bodily

fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

5 The tissue distribution of this gene in neutrophils indicates that the gene could be important for the treatment or detection of immune or hematopoietic disorders including arthritis, asthma, immunodeficiency diseases, leukemia, transplant rejection, and microbial infections. Expression of this gene product in immune cells indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of
10 potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene pr Protein, as well as, antibodies directed against the protein may show
15 utility as a tumor marker and/or immunotherapy targets for the above listed tissues. duct may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. In addition, this gene product may have commercial utility in the expansion
20 of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of
25 these sequences are related to SEQ ID NO:105 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the
30 general formula of a-b, where a is any integer between 1 to 641 of SEQ ID NO:105, b is an integer of 15 to 655, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:105, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 96

35

This gene is expressed primarily in osteosarcoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, osteosarcoma and other cancers. Similarly, polypeptides and antibodies
5 directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of bone, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. bone, cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma,
10 urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in osteosarcoma indicates that polynucleotides and
15 polypeptides corresponding to this gene are useful for the detection and treatment of: fracture and trauma, osteoporosis, osteosarcoma, osteoclastoma, chondrosarcoma, regulation of ossification and osteonecrosis, arthritis, tendonitis, chondromalacia and inflammation. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues.
20 Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:106 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome.
25 Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 592 of SEQ ID NO:106, b is an integer of 15 to 606, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:106, and where the b is greater than or equal to a + 14.

30

FEATURES OF PROTEIN ENCODED BY GENE NO: 97

This gene is expressed primarily in salivary gland and osteosarcoma.

Therefore, polynucleotides and polypeptides of the invention are useful as
35 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, osteosarcoma and other cancers, as well as digestive disorders.

Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of bone and the digestive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g., cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in osteosarcoma indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection and treatment of bone-related disorders and conditions, such as: fracture and trauma, osteoporosis, osteosarcoma, osteoclastoma, chondrosarcoma, regulation of ossification and osteonecrosis, arthritis, tendonitis, chondromalacia and inflammation. In addition, the expression in salivary gland suggest a possible role for this gene product in the detection and treatment of digestive disorders. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:107 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 643 of SEQ ID NO:107, b is an integer of 15 to 657, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:107, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 98

This gene is expressed primarily in neutrophils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, hematopoietic and immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoietic and immune systems,

expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. immune, cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in neutrophils indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of hematopoietic and immune disorders including: anemias, auto-immunities, immunodeficiencies (e.g. AIDS), immuno-suppressive conditions (transplantation) and leukemias. In addition this gene product may be applicable in conditions of general microbial infection, arthritis, inflammation or cancer. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:108 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 591 of SEQ ID NO:108, b is an integer of 15 to 605, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:108, and where the b is greater than or equal to a + 14.

25 FEATURES OF PROTEIN ENCODED BY GENE NO: 99

This gene is expressed primarily in breast lymph node.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, breast cancer and other immune diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. immune, cancerous and wounded tissues) or bodily fluids (e.g., lymph, breast milk, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or

cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in breast lymph node indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and intervention of breast cancer and other immune diseases. Expression of this gene product in lymph nodes indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:109 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 490 of SEQ ID NO:109, b is an integer of 15 to 504, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:109, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 100

This gene is expressed primarily in T-cell lymphoma, and to a lesser extent, in human thymus tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are

not limited to, T-cell lymphoma and immune diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues or cell types (e.g. immune, thymus, cancerous and wounded tissues) or bodily fluids (e.g., lymph, serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in T-cell lymphoma indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and intervention of T-cell lymphomas and other immune diseases. Expression of this gene product in the thymus, as well as in T-cell lymphomas, indicates a role in the regulation of the proliferation; survival; differentiation; and/or activation of potentially all hematopoietic cell lineages, including blood stem cells. This gene product may be involved in the regulation of cytokine production, antigen presentation, or other processes that may also suggest a usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the gene is expressed in cells of lymphoid origin, the natural gene product may be involved in immune functions. Therefore it may be also used as an agent for immunological disorders including arthritis, asthma, immune deficiency diseases such as AIDS, leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and psoriasis. In addition, this gene product may have commercial utility in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types. Protein, as well as, antibodies directed against the protein may show utility as a tumor marker and/or immunotherapy targets for the above listed tissues. . Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases. Some of these sequences are related to SEQ ID NO:110 and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 756 of SEQ ID NO:110, b is an integer of 15 to 770, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:110, and where the b is greater than or equal to a + 14.

FEATURES OF PROTEIN ENCODED BY GENE NO: 101

This gene is expressed primarily in chronic lymphocytic leukemia.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions which include, but are
not limited to, immune disorders, particularly chronic lymphocytic leukemia. Similarly,
polypeptides and antibodies directed to these polypeptides are useful in providing
immunological probes for differential identification of the tissue(s) or cell type(s). For a
10 number of disorders of the above tissues or cells, particularly of the hemapoietic system
expression of this gene at significantly higher or lower levels may be routinely detected
in certain tissues or cell types (e.g. immune, cancerous and wounded tissues) or bodily
fluids (e.g., serum, plasma, urine, synovial fluid and spinal fluid) or another tissue or
cell sample taken from an individual having such a disorder, relative to the standard
15 gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an
individual not having the disorder.

The tissue distribution in chronic lymphocytic leukemia indicates that
polynucleotides and polypeptides corresponding to this gene are useful for the
diagnosis and intervention of leukemia diseases or hemapoietic disorders. Expression of
20 this gene product in spleen indicates a role in the regulation of the proliferation;
survival; differentiation; and/or activation of potentially all hematopoietic cell lineages,
including blood stem cells. This gene product may be involved in the regulation of
cytokine production, antigen presentation, or other processes that may also suggest a
usefulness in the treatment of cancer (e.g. by boosting immune responses). Since the
25 gene is expressed in cells of lymphoid origin, the natural gene product may be involved
in immune functions. Therefore it may be also used as an agent for immunological
disorders including arthritis, asthma, immune deficiency diseases such as AIDS,
leukemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, and
psoriasis. In addition, this gene product may have commercial utility in the expansion
30 of stem cells and committed progenitors of various blood lineages, and in the
differentiation and/or proliferation of various cell types. Protein, as well as, antibodies
directed against the protein may show utility as a tumor marker and/or immunotherapy
targets for the above listed tissues. Many polynucleotide sequences, such as EST
sequences, are publicly available and accessible through sequence databases. Some of
35 these sequences are related to SEQ ID NO:111 and may have been publicly available
prior to conception of the present invention. Preferably, such related polynucleotides
are specifically excluded from the scope of the present invention. To list every related

sequence is cumbersome. Accordingly, preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 737 of SEQ ID NO:111, b is an integer of 15 to 751, where both a and b correspond to the positions of nucleotide
5 residues shown in SEQ ID NO:111, and where the b is greater than or equal to a + 14.

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
1	HCWCH14	209225 08/28/97	ZAP Express	11	552	65	552	183	113	1	29	30	86
1	HCWCH14	209225 08/28/97	ZAP Express	112	543	1	543	177	214	1	28	29	85
2	HE2EB74	209225 08/28/97	Uni-ZAP XR	12	1434	311	1418	507	114	1	16	17	19
3	HFGAD82	209225 08/28/97	Uni-ZAP XR	13	1881	772	1861	1019	115	1	18	19	38
4	HE9MI43	209225 08/28/97	Uni-ZAP XR	14	1060	1	1060	171	116	1	19	20	87
5	HE9NH44	209225 08/28/97	Uni-ZAP XR	15	1255	37	1255	113	117	1	18	19	38
6	HFKCK85	209225 08/28/97	Uni-ZAP XR	16	1036	1	1036	159	118	1	24	25	26

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
7	HHFCY66	209225 08/28/97	Uni-ZAP XR	17	1014	1	1014	49	49	119	1	19	20	21
8	HE2PI29	209225 08/28/97	Uni-ZAP XR	18	1287	1	1287	174	174	120	1	37	38	95
9	HE9AN21	209225 08/28/97	Uni-ZAP XR	19	1105	1	1105	327	327	121	1	22	23	35
10	HEPCE37	209225 08/28/97	Uni-ZAP XR	20	1089	1	1089	297	297	122	1	19	20	37
11	HLHDP83	209226 08/28/97	Uni-ZAP XR	21	2831	395	1598	426	426	123	1	36	37	341
12	HSIAS17	209226 08/28/97	Uni-ZAP XR	22	1448	1	1224	108	108	124	1	23	24	218
13	HSIEF95	209226 08/28/97	Uni-ZAP XR	23	1211	136	1211	177	177	125	1	25	26	265
14	HSDDC95	209226 08/28/97	Uni-ZAP XR	24	1060	1	1060	67	67	126	1	37	38	38

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
15	HOSDG32	209226 08/28/97	Uni-ZAP XR	25	1057	1	1057	175	175	127	1	21	22	92
16	HMUBU59	209226 08/28/97	pCMV Sport 3.0	26	980	1	980	30	30	128	1	41	42	195
17	HWTCE21	209226 08/28/97	Uni-ZAP XR	27	755	1	744	339	339	129	1	16	17	49
18	HFJUM15	209226 08/28/97	pSport1	28	946	1	946	168	168	130	1	32	33	54
19	HLYAN43	209226 08/28/97	pSport1	29	971	26	946	135	135	131	1	23	24	32
20	HBJFA56	209235 09/04/97	Uni-ZAP XR	30	1008	1	993	155	155	132	1	16	17	23
21	HTLAF13	209235 09/04/97	Uni-ZAP XR	31	990	80	990	164	164	133	1	26	27	219
22	HTLFI93	209235 09/04/97	Uni-ZAP XR	32	1131	1	1107	48	48	134	1	43	44	302

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
23	HBXGI20	209235 09/04/97	ZAP Express	33	1293	1	1002	199	199	135	1	37	38	40
24	HTPBH21	209235 09/04/97	Uni-ZAP XR	34	1014	1	1014	21	21	136	1	25	26	277
25	HSQAB87	209235 09/04/97	Uni-ZAP XR	35	1222	375	1222	473	473	137	1	19	20	110
26	HTEDJ94	209235 09/04/97	Uni-ZAP XR	36	901	1	901	240	240	138	1	46	47	132
27	HKMLM11	209236 09/04/97	pBluescript	37	954	1	954	82	82	139	1	20	21	130
28	HNEAC05	209236 09/04/97	Uni-ZAP XR	38	890	1	890	101	101	140	1	24	25	105
29	HETEW02	209236 09/04/97	Uni-ZAP XR	39	1070	1	905	98	98	141	1	19	20	61
30	HE8MG70	209236 09/04/97	Uni-ZAP XR	40	772	1	772	85	85	142	1	27	28	37

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
31	HLMCA59	209236 09/04/97	Uni-ZAP XR	41	787	1	787	101	101	143	1	31	32	63
32	HOAAC90	209236 09/04/97	Uni-ZAP XR	42	652	1	652	38	38	144	1	15	16	104
33	HMEJQ68	209236 09/04/97	Lambda ZAP II	43	1520	1	1520	89	89	145	1	37	38	60
34	HNGIJ31	209236 09/04/97	Uni-ZAP XR	44	796	1	796	135	135	146	1	16	17	36
35	HFXJZ18	209236 09/04/97	Lambda ZAP II	45	1378	436	1378	692	692	147	1	27	28	31
36	HPEBE79	209241 09/12/97	Uni-ZAP XR	46	597	1	597	79	79	148	1	13	14	15
37	HRTAE58	209241 09/12/97	pBluescript SK-	47	600	1	600	244	244	149	1	18	19	58
38	HSKNB54	209241 09/12/97	pBluescript	48	911	1	911	180	180	150	1	21	22	86

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
39	HSKNT34	209241 09/12/97	pBluescript	49	1863	1	1094	21	21	151	1	22	23	52
40	HTEDY42	209241 09/12/97	Uni-ZAP XR	50	810	1	810	19	19	152	1	23	24	77
41	HTLAA40	209241 09/12/97	Uni-ZAP XR	51	956	1	956	33	33	153	1	28	29	71
42	HTNBO91	209241 09/12/97	pBluescript SK-	52	300	1	300	7	7	154	1	26	27	40
43	H6BSD90	209241 09/12/97	Uni-ZAP XR	53	841	1	841	188	188	155	1	23	24	84
44	HBJBQ35	209241 09/12/97	Uni-ZAP XR	54	634	1	634	84	84	156	1	20	21	95
45	HCEIQ89	209242 09/12/97	Uni-ZAP XR	55	863	1	863	74	74	157	1	17	18	88
46	HCNSB61	209242 09/12/97	pBluescript	56	712	1	712	218	218	158	1	21	22	43

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
47	HCDBO20	209242 09/12/97	Uni-ZAP XR	57	925	1	925	8	8	159	1	42	43	45
48	HBNAW17	209242 09/12/97	Uni-ZAP XR	58	601	1	601	77	77	160	1	37	38	61
49	HCDBW86	209242 09/12/97	Uni-ZAP XR	59	730	1	730	139	139	161	1	20	21	30
50	HE6CL49	209242 09/12/97	Uni-ZAP XR	60	846	1	846	187	187	162	1			24
51	HEAAH81	209242 09/12/97	Uni-ZAP XR	61	958	1	958	224	224	163	1	23	24	70
52	HEBAE88	209242 09/12/97	Uni-ZAP XR	62	582	1	582	160	160	164	1	26	27	42
53	HFXGV31	209242 09/12/97	Lambda ZAP II	63	752	1	752	100	100	165	1	24	25	64
54	HEAAJ57	209242 09/12/97	Uni-ZAP XR	64	706	1	706	162	162	166	1	20	21	67

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	S' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
55	HCFMV71	209242 09/12/97	pSport1	65	400	1	400	31	31	167	1	24	25	58
56	HERAM05	209242 09/12/97	Uni-ZAP XR	66	773	1	773	240	240	168	1	14	15	53
57	HFKFY69	209242 09/12/97	Uni-ZAP XR	67	647	1	647	157	157	169	1			19
58	HFTCR15	209242 09/12/97	Uni-ZAP XR	68	675	1	675	82	82	170	1	28	29	38
59	HGBDL30	209242 09/12/97	Uni-ZAP XR	69	889	1	889	68	68	171	1	41	42	53
60	HFKEN81	209242 09/12/97	Uni-ZAP XR	70	888	1	888	25	25	172	1	23	24	54
61	HFPXC36	209242 09/12/97	Uni-ZAP XR	71	796	1	796	103	103	173	1	27	28	46
62	HFRAN90	209242 09/12/97	Uni-ZAP XR	72	532	1	532	178	178	174	1	39	40	54

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
63	HHGBO65	209242 09/12/97	Lambda ZAP II	73	546	1	546	279	279	175	1	25	26	26
64	HHGBO91	209242 09/12/97	Lambda ZAP II	74	715	1	715	140	140	176	1	28	29	49
65	HGLAL82	209242 09/12/97	Uni-ZAP XR	75	406	1	406	144	144	177	1	19	20	26
66	HERAN54	209242 09/12/97	Uni-ZAP XR	76	542	1	542	99	99	178	1	28	29	40
67	HFXDE67	209242 09/12/97	Lambda ZAP II	77	420	1	420	224	224	179	1	27	28	65
68	HFRAC19	209242 09/12/97	Uni-ZAP XR	78	465	1	465	146	146	180	1	17	18	19
69	HGLAJ51	209242 09/12/97	Uni-ZAP XR	79	890	1	890	212	212	181	1			14
70	HFFAD59	209242 09/12/97	Lambda ZAP II	80	470	1	470	44	44	182	1	17	18	45

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	5' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
71	HESAJ10	209242 09/12/97	Uni-ZAP XR	81	1090	400	1090	405	405	183	1	23	24	71
72	HMDAE65	209243 09/12/97	Uni-ZAP XR	82	698	1	698	179	179	184	1	17	18	77
73	HL YBV47	209243 09/12/97	pSport1	83	868	1	868	324	324	185	1	21	22	25
74	HMEGF92	209243 09/12/97	Lambda ZAP II	84	629	1	611	92	92	186	1	27	28	62
75	HNGIK36	209243 09/12/97	Uni-ZAP XR	85	837	1	837	48	48	187	1	41	42	91
76	HMEJJ27	209243 09/12/97	Lambda ZAP II	86	903	1	903	113	113	188	1	34	35	47
77	HNHCY64	209243 09/12/97	Uni-ZAP XR	87	725	1	725	258	258	189	1	34	35	44
78	HNHCY94	209243 09/12/97	Uni-ZAP XR	88	606	1	606	78	78	190	1	25	26	48

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
79	HNEBN76	209243 09/12/97	Uni-ZAP XR	89	1142	150	1142	346	346	191	1	24	25	81
80	HMEFT54	209243 09/12/97	Lambda ZAP II	90	596	1	596	332	332	192	1	24	25	39
81	HLQBE09	209243 09/12/97	Lambda ZAP II	91	633	1	633	17	17	193	1	19	20	181
82	HMWBC11	209243 09/12/97	Uni-Zap XR	92	725	1	725	139	139	194	1	28	29	39
83	HNGJR78	209243 09/12/97	Uni-ZAP XR	93	601	1	601	159	159	195	1	24	25	72
84	HNGDP26	209243 09/12/97	Uni-ZAP XR	94	692	1	692	77	77	196	1	21	22	55
85	HNGJH63	209243 09/12/97	Uni-ZAP XR	95	1005	1	1005	62	62	197	1	31	32	69
86	HMDAL04	209243 09/12/97	Uni-ZAP XR	96	612	1	612	48	48	198	1	21	22	46

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	5' NT of Clone Seq.	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
87	HMWHX28	209243 09/12/97	Uni-Zap XR	97	670	1	670	128	199	1	21	22	54
88	HNHAD65	209243 09/12/97	Uni-ZAP XR	98	619	1	619	27	200	1	22	23	37
89	HNGAP93	209243 09/12/97	Uni-ZAP XR	99	703	1	703	50	201	1	20	21	33
90	HNHCX60	209243 09/12/97	Uni-ZAP XR	100	762	1	762	158	202	1	21	22	21
91	HNHGB09	209243 09/12/97	Uni-ZAP XR	101	650	1	650	135	203	1	26	27	55
92	HNHHA15	209243 09/12/97	Uni-ZAP XR	102	360	1	360	11	204	1	32	33	116
93	HHGDC01	209243 09/12/97	Lambda Zap II	103	817	1	817	234	205	1	45	46	83
94	HMWGU74	209243 09/12/97	Uni-Zap XR	104	881	1	881	147	206	1	25	26	45

Gene No.	cDNA Clone ID	ATCC Deposit Nr and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	First AA of Secreted Portion	Last AA of ORF
95	HNGCF72	209243 09/12/97	Uni-ZAP XR	105	655	1	655	154	154	207	1	20	21	41
96	HOACB38	209243 09/12/97	Uni-ZAP XR	106	606	1	606	63	63	208	1	21	22	40
97	HOACG37	209243 09/12/97	Uni-ZAP XR	107	657	1	622	219	219	209	1	24	25	30
98	HNHBL26	209243 09/12/97	Uni-ZAP XR	108	605	1	605	195	195	210	1			11
99	HLMFD11	209243 09/12/97	Lambda ZAP II	109	504	1	504	40	40	211	1	31	32	99
100	HLTDV50	209243 09/12/97	Uni-ZAP XR	110	770	1	770	74	74	212	1	17	18	28
101	HL YBA22	209243 09/12/97	pSportI	111	751	1	751	153	153	213	1	31	32	46

Table 1 summarizes the information corresponding to each "Gene No." described above. The nucleotide sequence identified as "NT SEQ ID NO:X" was assembled from partially homologous ("overlapping") sequences obtained from the "cDNA clone ID" identified in Table 1 and, in some cases, from additional related DNA clones. The overlapping sequences were assembled into a single contiguous sequence of high redundancy (usually three to five overlapping sequences at each nucleotide position), resulting in a final sequence identified as SEQ ID NO:X.

The cDNA Clone ID was deposited on the date and given the corresponding deposit number listed in "ATCC Deposit No:Z and Date." Some of the deposits contain multiple different clones corresponding to the same gene. "Vector" refers to the type of vector contained in the cDNA Clone ID.

"Total NT Seq." refers to the total number of nucleotides in the contig identified by "Gene No." The deposited clone may contain all or most of these sequences, reflected by the nucleotide position indicated as "5' NT of Clone Seq." and the "3' NT of Clone Seq." of SEQ ID NO:X. The nucleotide position of SEQ ID NO:X of the putative start codon (methionine) is identified as "5' NT of Start Codon." Similarly, the nucleotide position of SEQ ID NO:X of the predicted signal sequence is identified as "5' NT of First AA of Signal Pep."

The translated amino acid sequence, beginning with the methionine, is identified as "AA SEQ ID NO:Y," although other reading frames can also be easily translated using known molecular biology techniques. The polypeptides produced by these alternative open reading frames are specifically contemplated by the present invention.

The first and last amino acid position of SEQ ID NO:Y of the predicted signal peptide is identified as "First AA of Sig Pep" and "Last AA of Sig Pep." The predicted first amino acid position of SEQ ID NO:Y of the secreted portion is identified as "Predicted First AA of Secreted Portion." Finally, the amino acid position of SEQ ID NO:Y of the last amino acid in the open reading frame is identified as "Last AA of ORF."

SEQ ID NO:X and the translated SEQ ID NO:Y are sufficiently accurate and otherwise suitable for a variety of uses well known in the art and described further below. For instance, SEQ ID NO:X is useful for designing nucleic acid hybridization probes that will detect nucleic acid sequences contained in SEQ ID NO:X or the cDNA contained in the deposited clone. These probes will also hybridize to nucleic acid molecules in biological samples, thereby enabling a variety of forensic and diagnostic methods of the invention. Similarly, polypeptides identified from SEQ ID NO:Y may

be used to generate antibodies which bind specifically to the secreted proteins encoded by the cDNA clones identified in Table 1.

Nevertheless, DNA sequences generated by sequencing reactions can contain sequencing errors. The errors exist as misidentified nucleotides, or as insertions or deletions of nucleotides in the generated DNA sequence. The erroneously inserted or deleted nucleotides cause frame shifts in the reading frames of the predicted amino acid sequence. In these cases, the predicted amino acid sequence diverges from the actual amino acid sequence, even though the generated DNA sequence may be greater than 99.9% identical to the actual DNA sequence (for example, one base insertion or deletion in an open reading frame of over 1000 bases).

Accordingly, for those applications requiring precision in the nucleotide sequence or the amino acid sequence, the present invention provides not only the generated nucleotide sequence identified as SEQ ID NO:X and the predicted translated amino acid sequence identified as SEQ ID NO:Y, but also a sample of plasmid DNA containing a human cDNA of the invention deposited with the ATCC, as set forth in Table 1. The nucleotide sequence of each deposited clone can readily be determined by sequencing the deposited clone in accordance with known methods. The predicted amino acid sequence can then be verified from such deposits. Moreover, the amino acid sequence of the protein encoded by a particular clone can also be directly determined by peptide sequencing or by expressing the protein in a suitable host cell containing the deposited human cDNA, collecting the protein, and determining its sequence.

The present invention also relates to the genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, or the deposited clone. The corresponding gene can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include preparing probes or primers from the disclosed sequence and identifying or amplifying the corresponding gene from appropriate sources of genomic material.

Also provided in the present invention are species homologs. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source for the desired homologue.

The polypeptides of the invention can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced polypeptides, or polypeptides produced by a combination of these methods. Means for preparing such polypeptides are well understood in the art.

The polypeptides may be in the form of the secreted protein, including the mature form, or may be a part of a larger protein, such as a fusion protein (see below). It is often advantageous to include an additional amino acid sequence which contains secretory or leader sequences, pro-sequences, sequences which aid in purification ,
5 such as multiple histidine residues, or an additional sequence for stability during recombinant production.

The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of a polypeptide, including the secreted polypeptide, can be substantially purified by the
10 one-step method described in Smith and Johnson, Gene 67:31-40 (1988). Polypeptides of the invention also can be purified from natural or recombinant sources using antibodies of the invention raised against the secreted protein in methods which are well known in the art.

15 Signal Sequences

Methods for predicting whether a protein has a signal sequence, as well as the cleavage point for that sequence, are available. For instance, the method of McGeoch, Virus Res. 3:271-286 (1985), uses the information from a short N-terminal charged region and a subsequent uncharged region of the complete (uncleaved) protein. The
20 method of von Heinje, Nucleic Acids Res. 14:4683-4690 (1986) uses the information from the residues surrounding the cleavage site, typically residues -13 to +2, where +1 indicates the amino terminus of the secreted protein. The accuracy of predicting the cleavage points of known mammalian secretory proteins for each of these methods is in the range of 75-80%. (von Heinje, supra.) However, the two methods do not always
25 produce the same predicted cleavage point(s) for a given protein.

In the present case, the deduced amino acid sequence of the secreted polypeptide was analyzed by a computer program called SignalP (Henrik Nielsen et al., Protein Engineering 10:1-6 (1997)), which predicts the cellular location of a protein based on the amino acid sequence. As part of this computational prediction of localization, the
30 methods of McGeoch and von Heinje are incorporated. The analysis of the amino acid sequences of the secreted proteins described herein by this program provided the results shown in Table 1.

As one of ordinary skill would appreciate, however, cleavage sites sometimes vary from organism to organism and cannot be predicted with absolute certainty.
35 Accordingly, the present invention provides secreted polypeptides having a sequence shown in SEQ ID NO:Y which have an N-terminus beginning within 5 residues (i.e., + or - 5 residues) of the predicted cleavage point. Similarly, it is also recognized that in

some cases, cleavage of the signal sequence from a secreted protein is not entirely uniform, resulting in more than one secreted species. These polypeptides, and the polynucleotides encoding such polypeptides, are contemplated by the present invention.

Moreover, the signal sequence identified by the above analysis may not necessarily predict the naturally occurring signal sequence. For example, the naturally occurring signal sequence may be further upstream from the predicted signal sequence. However, it is likely that the predicted signal sequence will be capable of directing the secreted protein to the ER. These polypeptides, and the polynucleotides encoding such polypeptides, are contemplated by the present invention.

Polynucleotide and Polypeptide Variants

"Variant" refers to a polynucleotide or polypeptide differing from the polynucleotide or polypeptide of the present invention, but retaining essential properties thereof. Generally, variants are overall closely similar, and, in many regions, identical to the polynucleotide or polypeptide of the present invention.

By a polynucleotide having a nucleotide sequence at least, for example, 95% "identical" to a reference nucleotide sequence of the present invention, it is intended that the nucleotide sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence encoding the polypeptide. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. The query sequence may be an entire sequence shown in Table 1, the ORF (open reading frame), or any fragment specified as described herein.

As a practical matter, whether any particular nucleic acid molecule or polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleotide sequence of the present invention can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci. (1990) 6:237-245). In a sequence alignment the query and subject sequences are both DNA sequences. An RNA sequence can be compared by converting U's to T's. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB alignment of DNA sequences to calculate percent identity are:

Matrix=Unitary, k-tuple=4, Mismatch Penalty=1, Joining Penalty=30, Randomization Group Length=0, Cutoff Score=1, Gap Penalty=5, Gap Size Penalty 0.05, Window Size=500 or the length of the subject nucleotide sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence because of 5' or 3' deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for 5' and 3' truncations of the subject sequence when calculating percent identity. For subject sequences truncated at the 5' or 3' ends, relative to the query sequence, the percent identity is corrected by calculating the number of bases of the query sequence that are 5' and 3' of the subject sequence, which are not matched/aligned, as a percent of the total bases of the query sequence. Whether a nucleotide is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This corrected score is what is used for the purposes of the present invention. Only bases outside the 5' and 3' bases of the subject sequence, as displayed by the FASTDB alignment, which are not matched/aligned with the query sequence, are calculated for the purposes of manually adjusting the percent identity score.

For example, a 90 base subject sequence is aligned to a 100 base query sequence to determine percent identity. The deletions occur at the 5' end of the subject sequence and therefore, the FASTDB alignment does not show a matched/alignment of the first 10 bases at 5' end. The 10 unpaired bases represent 10% of the sequence (number of bases at the 5' and 3' ends not matched/total number of bases in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 bases were perfectly matched the final percent identity would be 90%. In another example, a 90 base subject sequence is compared with a 100 base query sequence. This time the deletions are internal deletions so that there are no bases on the 5' or 3' of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only bases 5' and 3' of the subject sequence which are not matched/aligned with the query sequence are manually corrected for. No other manual corrections are to be made for the purposes of the present invention.

By a polypeptide having an amino acid sequence at least, for example, 95% "identical" to a query amino acid sequence of the present invention, it is intended that the amino acid sequence of the subject polypeptide is identical to the query sequence except that the subject polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the query amino acid sequence. In other words,

to obtain a polypeptide having an amino acid sequence at least 95% identical to a query amino acid sequence, up to 5% of the amino acid residues in the subject sequence may be inserted, deleted, (indels) or substituted with another amino acid. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular polypeptide is at least 90%, 95%, 96%, 97%, 98% or 99% identical to, for instance, the amino acid sequences shown in Table 1 or to the amino acid sequence encoded by deposited DNA clone can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci. (1990) 6:237-245). In a sequence alignment the query and subject sequences are either both nucleotide sequences or both amino acid sequences. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB amino acid alignment are: Matrix=PAM 0, k-tuple=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group Length=0, Cutoff Score=1, Window Size=sequence length, Gap Penalty=5, Gap Size Penalty=0.05, Window Size=500 or the length of the subject amino acid sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence due to N- or C-terminal deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for N- and C-terminal truncations of the subject sequence when calculating global percent identity. For subject sequences truncated at the N- and C-termini, relative to the query sequence, the percent identity is corrected by calculating the number of residues of the query sequence that are N- and C-terminal of the subject sequence, which are not matched/aligned with a corresponding subject residue, as a percent of the total bases of the query sequence. Whether a residue is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This final percent identity score is what is used for the purposes of the present invention. Only residues to the N- and C-termini of the subject sequence, which are not matched/aligned with the query sequence, are considered for the purposes of manually adjusting the percent identity score. That is, only query residue positions outside the farthest N- and C-terminal residues of the

subject sequence.

For example, a 90 amino acid residue subject sequence is aligned with a 100 residue query sequence to determine percent identity. The deletion occurs at the N-terminus of the subject sequence and therefore, the FASTDB alignment does not show a matching/alignment of the first 10 residues at the N-terminus. The 10 unpaired residues represent 10% of the sequence (number of residues at the N- and C- termini not matched/total number of residues in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 residues were perfectly matched the final percent identity would be 90%. In another example, a 90 residue subject sequence is compared with a 100 residue query sequence. This time the deletions are internal deletions so there are no residues at the N- or C-termini of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only residue positions outside the N- and C-terminal ends of the subject sequence, as displayed in the FASTDB alignment, which are not matched/aligned with the query sequence are manually corrected for. No other manual corrections are to be made for the purposes of the present invention.

The variants may contain alterations in the coding regions, non-coding regions, or both. Especially preferred are polynucleotide variants containing alterations which produce silent substitutions, additions, or deletions, but do not alter the properties or activities of the encoded polypeptide. Nucleotide variants produced by silent substitutions due to the degeneracy of the genetic code are preferred. Moreover, variants in which 5-10, 1-5, or 1-2 amino acids are substituted, deleted, or added in any combination are also preferred. Polynucleotide variants can be produced for a variety of reasons, e.g., to optimize codon expression for a particular host (change codons in the human mRNA to those preferred by a bacterial host such as *E. coli*).

Naturally occurring variants are called "allelic variants," and refer to one of several alternate forms of a gene occupying a given locus on a chromosome of an organism. (Genes II, Lewin, B., ed., John Wiley & Sons, New York (1985).) These allelic variants can vary at either the polynucleotide and/or polypeptide level. Alternatively, non-naturally occurring variants may be produced by mutagenesis techniques or by direct synthesis.

Using known methods of protein engineering and recombinant DNA technology, variants may be generated to improve or alter the characteristics of the polypeptides of the present invention. For instance, one or more amino acids can be deleted from the N-terminus or C-terminus of the secreted protein without substantial loss of biological function. The authors of Ron et al., *J. Biol. Chem.* 268: 2984-2988

(1993), reported variant KGF proteins having heparin binding activity even after deleting 3, 8, or 27 amino-terminal amino acid residues. Similarly, Interferon gamma exhibited up to ten times higher activity after deleting 8-10 amino acid residues from the carboxy terminus of this protein. (Dobeli et al., J. Biotechnology 7:199-216 (1988).)

5 Moreover, ample evidence demonstrates that variants often retain a biological activity similar to that of the naturally occurring protein. For example, Gayle and coworkers (J. Biol. Chem 268:22105-22111 (1993)) conducted extensive mutational analysis of human cytokine IL-1a. They used random mutagenesis to generate over 3,500 individual IL-1a mutants that averaged 2.5 amino acid changes per variant over
10 the entire length of the molecule. Multiple mutations were examined at every possible amino acid position. The investigators found that "[m]ost of the molecule could be altered with little effect on either [binding or biological activity]." (See, Abstract.) In fact, only 23 unique amino acid sequences, out of more than 3,500 nucleotide sequences examined, produced a protein that significantly differed in activity from wild-
15 type.

 Furthermore, even if deleting one or more amino acids from the N-terminus or C-terminus of a polypeptide results in modification or loss of one or more biological functions, other biological activities may still be retained. For example, the ability of a deletion variant to induce and/or to bind antibodies which recognize the secreted form
20 will likely be retained when less than the majority of the residues of the secreted form are removed from the N-terminus or C-terminus. Whether a particular polypeptide lacking N- or C-terminal residues of a protein retains such immunogenic activities can readily be determined by routine methods described herein and otherwise known in the art.

25 Thus, the invention further includes polypeptide variants which show substantial biological activity. Such variants include deletions, insertions, inversions, repeats, and substitutions selected according to general rules known in the art so as have little effect on activity. For example, guidance concerning how to make phenotypically silent amino acid substitutions is provided in Bowie, J. U. et al.,
30 Science 247:1306-1310 (1990), wherein the authors indicate that there are two main strategies for studying the tolerance of an amino acid sequence to change.

 The first strategy exploits the tolerance of amino acid substitutions by natural selection during the process of evolution. By comparing amino acid sequences in different species, conserved amino acids can be identified. These conserved amino
35 acids are likely important for protein function. In contrast, the amino acid positions where substitutions have been tolerated by natural selection indicates that these

positions are not critical for protein function. Thus, positions tolerating amino acid substitution could be modified while still maintaining biological activity of the protein.

The second strategy uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene to identify regions critical for protein function. For example, site directed mutagenesis or alanine-scanning mutagenesis (introduction of single alanine mutations at every residue in the molecule) can be used. (Cunningham and Wells, Science 244:1081-1085 (1989).) The resulting mutant molecules can then be tested for biological activity.

As the authors state, these two strategies have revealed that proteins are surprisingly tolerant of amino acid substitutions. The authors further indicate which amino acid changes are likely to be permissive at certain amino acid positions in the protein. For example, most buried (within the tertiary structure of the protein) amino acid residues require nonpolar side chains, whereas few features of surface side chains are generally conserved. Moreover, tolerated conservative amino acid substitutions involve replacement of the aliphatic or hydrophobic amino acids Ala, Val, Leu and Ile; replacement of the hydroxyl residues Ser and Thr; replacement of the acidic residues Asp and Glu; replacement of the amide residues Asn and Gln, replacement of the basic residues Lys, Arg, and His; replacement of the aromatic residues Phe, Tyr, and Trp, and replacement of the small-sized amino acids Ala, Ser, Thr, Met, and Gly.

Besides conservative amino acid substitution, variants of the present invention include (i) substitutions with one or more of the non-conserved amino acid residues, where the substituted amino acid residues may or may not be one encoded by the genetic code, or (ii) substitution with one or more of amino acid residues having a substituent group, or (iii) fusion of the mature polypeptide with another compound, such as a compound to increase the stability and/or solubility of the polypeptide (for example, polyethylene glycol), or (iv) fusion of the polypeptide with additional amino acids, such as an IgG Fc fusion region peptide, or leader or secretory sequence, or a sequence facilitating purification. Such variant polypeptides are deemed to be within the scope of those skilled in the art from the teachings herein.

For example, polypeptide variants containing amino acid substitutions of charged amino acids with other charged or neutral amino acids may produce proteins with improved characteristics, such as less aggregation. Aggregation of pharmaceutical formulations both reduces activity and increases clearance due to the aggregate's immunogenic activity. (Pinckard et al., Clin. Exp. Immunol. 2:331-340 (1967); Robbins et al., Diabetes 36: 838-845 (1987); Cleland et al., Crit. Rev. Therapeutic Drug Carrier Systems 10:307-377 (1993).)

Polynucleotide and Polypeptide Fragments

In the present invention, a "polynucleotide fragment" refers to a short polynucleotide having a nucleic acid sequence contained in the deposited clone or shown in SEQ ID NO:X. The short nucleotide fragments are preferably at least about 15 nt, and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nt in length. A fragment "at least 20 nt in length," for example, is intended to include 20 or more contiguous bases from the cDNA sequence contained in the deposited clone or the nucleotide sequence shown in SEQ ID NO:X. These nucleotide fragments are useful as diagnostic probes and primers as discussed herein. Of course, larger fragments (e.g., 50, 150, 500, 600, 2000 nucleotides) are preferred.

Moreover, representative examples of polynucleotide fragments of the invention, include, for example, fragments having a sequence from about nucleotide number 1-50, 51-100, 101-150, 151-200, 201-250, 251-300, 301-350, 351-400, 401-450, 451-500, 501-550, 551-600, 651-700, 701-750, 751-800, 800-850, 851-900, 901-950, 951-1000, 1001-1050, 1051-1100, 1101-1150, 1151-1200, 1201-1250, 1251-1300, 1301-1350, 1351-1400, 1401-1450, 1451-1500, 1501-1550, 1551-1600, 1601-1650, 1651-1700, 1701-1750, 1751-1800, 1801-1850, 1851-1900, 1901-1950, 1951-2000, or 2001 to the end of SEQ ID NO:X or the cDNA contained in the deposited clone. In this context "about" includes the particularly recited ranges, larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Preferably, these fragments encode a polypeptide which has biological activity. More preferably, these polynucleotides can be used as probes or primers as discussed herein.

In the present invention, a "polypeptide fragment" refers to a short amino acid sequence contained in SEQ ID NO:Y or encoded by the cDNA contained in the deposited clone. Protein fragments may be "free-standing," or comprised within a larger polypeptide of which the fragment forms a part or region, most preferably as a single continuous region. Representative examples of polypeptide fragments of the invention, include, for example, fragments from about amino acid number 1-20, 21-40, 41-60, 61-80, 81-100, 102-120, 121-140, 141-160, or 161 to the end of the coding region. Moreover, polypeptide fragments can be about 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, or 150 amino acids in length. In this context "about" includes the particularly recited ranges, larger or smaller by several (5, 4, 3, 2, or 1) amino acids, at either extreme or at both extremes.

Preferred polypeptide fragments include the secreted protein as well as the mature form. Further preferred polypeptide fragments include the secreted protein or

the mature form having a continuous series of deleted residues from the amino or the carboxy terminus, or both. For example, any number of amino acids, ranging from 1-60, can be deleted from the amino terminus of either the secreted polypeptide or the mature form. Similarly, any number of amino acids, ranging from 1-30, can be deleted from the carboxy terminus of the secreted protein or mature form. Furthermore, any combination of the above amino and carboxy terminus deletions are preferred. Similarly, polynucleotide fragments encoding these polypeptide fragments are also preferred.

Also preferred are polypeptide and polynucleotide fragments characterized by structural or functional domains, such as fragments that comprise alpha-helix and alpha-helix forming regions, beta-sheet and beta-sheet-forming regions, turn and turn-forming regions, coil and coil-forming regions, hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta amphipathic regions, flexible regions, surface-forming regions, substrate binding region, and high antigenic index regions. Polypeptide fragments of SEQ ID NO:Y falling within conserved domains are specifically contemplated by the present invention. Moreover, polynucleotide fragments encoding these domains are also contemplated.

Other preferred fragments are biologically active fragments. Biologically active fragments are those exhibiting activity similar, but not necessarily identical, to an activity of the polypeptide of the present invention. The biological activity of the fragments may include an improved desired activity, or a decreased undesirable activity.

Epitopes & Antibodies

In the present invention, "epitopes" refer to polypeptide fragments having antigenic or immunogenic activity in an animal, especially in a human. A preferred embodiment of the present invention relates to a polypeptide fragment comprising an epitope, as well as the polynucleotide encoding this fragment. A region of a protein molecule to which an antibody can bind is defined as an "antigenic epitope." In contrast, an "immunogenic epitope" is defined as a part of a protein that elicits an antibody response. (See, for instance, Geysen et al., Proc. Natl. Acad. Sci. USA 81:3998-4002 (1983).)

Fragments which function as epitopes may be produced by any conventional means. (See, e.g., Houghten, R. A., Proc. Natl. Acad. Sci. USA 82:5131-5135 (1985) further described in U.S. Patent No. 4,631,211.)

In the present invention, antigenic epitopes preferably contain a sequence of at least seven, more preferably at least nine, and most preferably between about 15 to about 30 amino acids. Antigenic epitopes are useful to raise antibodies, including

monoclonal antibodies, that specifically bind the epitope. (See, for instance, Wilson et al., Cell 37:767-778 (1984); Sutcliffe, J. G. et al., Science 219:660-666 (1983).)

Similarly, immunogenic epitopes can be used to induce antibodies according to methods well known in the art. (See, for instance, Sutcliffe et al., supra; Wilson et al., supra; Chow, M. et al., Proc. Natl. Acad. Sci. USA 82:910-914; and Bittle, F. J. et al., J. Gen. Virol. 66:2347-2354 (1985).) A preferred immunogenic epitope includes the secreted protein. The immunogenic epitopes may be presented together with a carrier protein, such as an albumin, to an animal system (such as rabbit or mouse) or, if it is long enough (at least about 25 amino acids), without a carrier. However, immunogenic epitopes comprising as few as 8 to 10 amino acids have been shown to be sufficient to raise antibodies capable of binding to, at the very least, linear epitopes in a denatured polypeptide (e.g., in Western blotting.)

As used herein, the term "antibody" (Ab) or "monoclonal antibody" (Mab) is meant to include intact molecules as well as antibody fragments (such as, for example, Fab and F(ab')₂ fragments) which are capable of specifically binding to protein. Fab and F(ab')₂ fragments lack the Fc fragment of intact antibody, clear more rapidly from the circulation, and may have less non-specific tissue binding than an intact antibody. (Wahl et al., J. Nucl. Med. 24:316-325 (1983).) Thus, these fragments are preferred, as well as the products of a FAB or other immunoglobulin expression library. Moreover, antibodies of the present invention include chimeric, single chain, and humanized antibodies.

Fusion Proteins

Any polypeptide of the present invention can be used to generate fusion proteins. For example, the polypeptide of the present invention, when fused to a second protein, can be used as an antigenic tag. Antibodies raised against the polypeptide of the present invention can be used to indirectly detect the second protein by binding to the polypeptide. Moreover, because secreted proteins target cellular locations based on trafficking signals, the polypeptides of the present invention can be used as targeting molecules once fused to other proteins.

Examples of domains that can be fused to polypeptides of the present invention include not only heterologous signal sequences, but also other heterologous functional regions. The fusion does not necessarily need to be direct, but may occur through linker sequences.

Moreover, fusion proteins may also be engineered to improve characteristics of the polypeptide of the present invention. For instance, a region of additional amino acids, particularly charged amino acids, may be added to the N-terminus of the

polypeptide to improve stability and persistence during purification from the host cell or subsequent handling and storage. Also, peptide moieties may be added to the polypeptide to facilitate purification. Such regions may be removed prior to final preparation of the polypeptide. The addition of peptide moieties to facilitate handling of polypeptides are familiar and routine techniques in the art.

Moreover, polypeptides of the present invention, including fragments, and specifically epitopes, can be combined with parts of the constant domain of immunoglobulins (IgG), resulting in chimeric polypeptides. These fusion proteins facilitate purification and show an increased half-life in vivo. One reported example describes chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins. (EP A 394,827; Traunecker et al., *Nature* 331:84-86 (1988).) Fusion proteins having disulfide-linked dimeric structures (due to the IgG) can also be more efficient in binding and neutralizing other molecules, than the monomeric secreted protein or protein fragment alone. (Fountoulakis et al., *J. Biochem.* 270:3958-3964 (1995).)

Similarly, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion proteins comprising various portions of constant region of immunoglobulin molecules together with another human protein or part thereof. In many cases, the Fc part in a fusion protein is beneficial in therapy and diagnosis, and thus can result in, for example, improved pharmacokinetic properties. (EP-A 0232 262.) Alternatively, deleting the Fc part after the fusion protein has been expressed, detected, and purified, would be desired. For example, the Fc portion may hinder therapy and diagnosis if the fusion protein is used as an antigen for immunizations. In drug discovery, for example, human proteins, such as hIL-5, have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. (See, D. Bennett et al., *J. Molecular Recognition* 8:52-58 (1995); K. Johanson et al., *J. Biol. Chem.* 270:9459-9471 (1995).)

Moreover, the polypeptides of the present invention can be fused to marker sequences, such as a peptide which facilitates purification of the fused polypeptide. In preferred embodiments, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311), among others, many of which are commercially available. As described in Gentz et al., *Proc. Natl. Acad. Sci. USA* 86:821-824 (1989), for instance, hexa-histidine provides for convenient purification of the fusion protein. Another peptide tag useful for purification, the "HA" tag, corresponds to an epitope derived from the influenza hemagglutinin protein. (Wilson et al., *Cell* 37:767 (1984).)

Thus, any of these above fusions can be engineered using the polynucleotides or the polypeptides of the present invention.

Vectors, Host Cells, and Protein Production

5 The present invention also relates to vectors containing the polynucleotide of the present invention, host cells, and the production of polypeptides by recombinant techniques. The vector may be, for example, a phage, plasmid, viral, or retroviral vector. Retroviral vectors may be replication competent or replication defective. In the latter case, viral propagation generally will occur only in complementing host cells.

10 The polynucleotides may be joined to a vector containing a selectable marker for propagation in a host. Generally, a plasmid vector is introduced in a precipitate, such as a calcium phosphate precipitate, or in a complex with a charged lipid. If the vector is a virus, it may be packaged in vitro using an appropriate packaging cell line and then transduced into host cells.

15 The polynucleotide insert should be operatively linked to an appropriate promoter, such as the phage lambda PL promoter, the E. coli lac, trp, phoA and tac promoters, the SV40 early and late promoters and promoters of retroviral LTRs, to name a few. Other suitable promoters will be known to the skilled artisan. The expression constructs will further contain sites for transcription initiation, termination,
20 and, in the transcribed region, a ribosome binding site for translation. The coding portion of the transcripts expressed by the constructs will preferably include a translation initiating codon at the beginning and a termination codon (UAA, UGA or UAG) appropriately positioned at the end of the polypeptide to be translated.

 As indicated, the expression vectors will preferably include at least one
25 selectable marker. Such markers include dihydrofolate reductase, G418 or neomycin resistance for eukaryotic cell culture and tetracycline, kanamycin or ampicillin resistance genes for culturing in E. coli and other bacteria. Representative examples of appropriate hosts include, but are not limited to, bacterial cells, such as E. coli, Streptomyces and Salmonella typhimurium cells; fungal cells, such as yeast cells; insect
30 cells such as Drosophila S2 and Spodoptera Sf9 cells; animal cells such as CHO, COS, 293, and Bowes melanoma cells; and plant cells. Appropriate culture mediums and conditions for the above-described host cells are known in the art.

 Among vectors preferred for use in bacteria include pQE70, pQE60 and pQE-9, available from QIAGEN, Inc.; pBluescript vectors, Phagescript vectors, pNH8A,
35 pNH16a, pNH18A, pNH46A, available from Stratagene Cloning Systems, Inc.; and ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 available from Pharmacia Biotech, Inc. Among preferred eukaryotic vectors are pWLNEO, pSV2CAT, pOG44, pXT1

and pSG available from Stratagene; and pSVK3, pBPV, pMSG and pSVL available from Pharmacia. Other suitable vectors will be readily apparent to the skilled artisan.

Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection, or other methods. Such methods are described in many standard laboratory manuals, such as Davis et al., Basic Methods In Molecular Biology (1986). It is specifically contemplated that the polypeptides of the present invention may in fact be expressed by a host cell lacking a recombinant vector.

A polypeptide of this invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography ("HPLC") is employed for purification.

Polypeptides of the present invention, and preferably the secreted form, can also be recovered from: products purified from natural sources, including bodily fluids, tissues and cells, whether directly isolated or cultured; products of chemical synthetic procedures; and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast, higher plant, insect, and mammalian cells. Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated or may be non-glycosylated. In addition, polypeptides of the invention may also include an initial modified methionine residue, in some cases as a result of host-mediated processes. Thus, it is well known in the art that the N-terminal methionine encoded by the translation initiation codon generally is removed with high efficiency from any protein after translation in all eukaryotic cells. While the N-terminal methionine on most proteins also is efficiently removed in most prokaryotes, for some proteins, this prokaryotic removal process is inefficient, depending on the nature of the amino acid to which the N-terminal methionine is covalently linked.

Uses of the Polynucleotides

Each of the polynucleotides identified herein can be used in numerous ways as reagents. The following description should be considered exemplary and utilizes known techniques.

The polynucleotides of the present invention are useful for chromosome identification. There exists an ongoing need to identify new chromosome markers,

since few chromosome marking reagents, based on actual sequence data (repeat polymorphisms), are presently available. Each polynucleotide of the present invention can be used as a chromosome marker.

5 Briefly, sequences can be mapped to chromosomes by preparing PCR primers (preferably 15-25 bp) from the sequences shown in SEQ ID NO:X. Primers can be selected using computer analysis so that primers do not span more than one predicted exon in the genomic DNA. These primers are then used for PCR screening of somatic cell hybrids containing individual human chromosomes. Only those hybrids containing the human gene corresponding to the SEQ ID NO:X will yield an amplified fragment.

10 Similarly, somatic hybrids provide a rapid method of PCR mapping the polynucleotides to particular chromosomes. Three or more clones can be assigned per day using a single thermal cycler. Moreover, sublocalization of the polynucleotides can be achieved with panels of specific chromosome fragments. Other gene mapping strategies that can be used include in situ hybridization, prescreening with labeled flow-
15 sorted chromosomes, and preselection by hybridization to construct chromosome specific-cDNA libraries.

Precise chromosomal location of the polynucleotides can also be achieved using fluorescence in situ hybridization (FISH) of a metaphase chromosomal spread. This technique uses polynucleotides as short as 500 or 600 bases; however, polynucleotides
20 2,000-4,000 bp are preferred. For a review of this technique, see Verma et al., "Human Chromosomes: a Manual of Basic Techniques," Pergamon Press, New York (1988).

For chromosome mapping, the polynucleotides can be used individually (to mark a single chromosome or a single site on that chromosome) or in panels (for
25 marking multiple sites and/or multiple chromosomes). Preferred polynucleotides correspond to the noncoding regions of the cDNAs because the coding sequences are more likely conserved within gene families, thus increasing the chance of cross hybridization during chromosomal mapping.

Once a polynucleotide has been mapped to a precise chromosomal location, the
30 physical position of the polynucleotide can be used in linkage analysis. Linkage analysis establishes coinheritance between a chromosomal location and presentation of a particular disease. (Disease mapping data are found, for example, in V. McKusick, Mendelian Inheritance in Man (available on line through Johns Hopkins University Welch Medical Library) .) Assuming 1 megabase mapping resolution and one gene per
35 20 kb, a cDNA precisely localized to a chromosomal region associated with the disease could be one of 50-500 potential causative genes.

Thus, once coinheritance is established, differences in the polynucleotide and the corresponding gene between affected and unaffected individuals can be examined. First, visible structural alterations in the chromosomes, such as deletions or translocations, are examined in chromosome spreads or by PCR. If no structural alterations exist, the presence of point mutations are ascertained. Mutations observed in some or all affected individuals, but not in normal individuals, indicates that the mutation may cause the disease. However, complete sequencing of the polypeptide and the corresponding gene from several normal individuals is required to distinguish the mutation from a polymorphism. If a new polymorphism is identified, this polymorphic polypeptide can be used for further linkage analysis.

Furthermore, increased or decreased expression of the gene in affected individuals as compared to unaffected individuals can be assessed using polynucleotides of the present invention. Any of these alterations (altered expression, chromosomal rearrangement, or mutation) can be used as a diagnostic or prognostic marker.

In addition to the foregoing, a polynucleotide can be used to control gene expression through triple helix formation or antisense DNA or RNA. Both methods rely on binding of the polynucleotide to DNA or RNA. For these techniques, preferred polynucleotides are usually 20 to 40 bases in length and complementary to either the region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxy-nucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988).) Triple helix formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques are effective in model systems, and the information disclosed herein can be used to design antisense or triple helix polynucleotides in an effort to treat disease.

Polynucleotides of the present invention are also useful in gene therapy. One goal of gene therapy is to insert a normal gene into an organism having a defective gene, in an effort to correct the genetic defect. The polynucleotides disclosed in the present invention offer a means of targeting such genetic defects in a highly accurate manner. Another goal is to insert a new gene that was not present in the host genome, thereby producing a new trait in the host cell.

The polynucleotides are also useful for identifying individuals from minute biological samples. The United States military, for example, is considering the use of restriction fragment length polymorphism (RFLP) for identification of its personnel. In

this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identifying personnel. This method does not suffer from the current limitations of "Dog Tags" which can be lost, switched, or stolen, making positive identification difficult. The polynucleotides of the present invention can be used as additional DNA markers for RFLP.

The polynucleotides of the present invention can also be used as an alternative to RFLP, by determining the actual base-by-base DNA sequence of selected portions of an individual's genome. These sequences can be used to prepare PCR primers for amplifying and isolating such selected DNA, which can then be sequenced. Using this technique, individuals can be identified because each individual will have a unique set of DNA sequences. Once an unique ID database is established for an individual, positive identification of that individual, living or dead, can be made from extremely small tissue samples.

Forensic biology also benefits from using DNA-based identification techniques as disclosed herein. DNA sequences taken from very small biological samples such as tissues, e.g., hair or skin, or body fluids, e.g., blood, saliva, semen, etc., can be amplified using PCR. In one prior art technique, gene sequences amplified from polymorphic loci, such as DQa class II HLA gene, are used in forensic biology to identify individuals. (Erich, H., PCR Technology, Freeman and Co. (1992).) Once these specific polymorphic loci are amplified, they are digested with one or more restriction enzymes, yielding an identifying set of bands on a Southern blot probed with DNA corresponding to the DQa class II HLA gene. Similarly, polynucleotides of the present invention can be used as polymorphic markers for forensic purposes.

There is also a need for reagents capable of identifying the source of a particular tissue. Such need arises, for example, in forensics when presented with tissue of unknown origin. Appropriate reagents can comprise, for example, DNA probes or primers specific to particular tissue prepared from the sequences of the present invention. Panels of such reagents can identify tissue by species and/or by organ type. In a similar fashion, these reagents can be used to screen tissue cultures for contamination.

In the very least, the polynucleotides of the present invention can be used as molecular weight markers on Southern gels, as diagnostic probes for the presence of a specific mRNA in a particular cell type, as a probe to "subtract-out" known sequences in the process of discovering novel polynucleotides, for selecting and making oligomers for attachment to a "gene chip" or other support, to raise anti-DNA antibodies using DNA immunization techniques, and as an antigen to elicit an immune response.

Uses of the Polypeptides

Each of the polypeptides identified herein can be used in numerous ways. The following description should be considered exemplary and utilizes known techniques.

5 A polypeptide of the present invention can be used to assay protein levels in a biological sample using antibody-based techniques. For example, protein expression in tissues can be studied with classical immunohistological methods. (Jalkanen, M., et al., J. Cell. Biol. 101:976-985 (1985); Jalkanen, M., et al., J. Cell. Biol. 105:3087-3096 (1987).) Other antibody-based methods useful for detecting protein gene
10 expression include immunoassays, such as the enzyme linked immunosorbent assay (ELISA) and the radioimmunoassay (RIA). Suitable antibody assay labels are known in the art and include enzyme labels, such as, glucose oxidase, and radioisotopes, such as iodine (^{125}I , ^{121}I), carbon (^{14}C), sulfur (^{35}S), tritium (^3H), indium (^{112}In), and technetium ($^{99\text{m}}\text{Tc}$), and fluorescent labels, such as fluorescein and rhodamine, and
15 biotin.

In addition to assaying secreted protein levels in a biological sample, proteins can also be detected in vivo by imaging. Antibody labels or markers for in vivo imaging of protein include those detectable by X-radiography, NMR or ESR. For X-radiography, suitable labels include radioisotopes such as barium or cesium, which emit
20 detectable radiation but are not overtly harmful to the subject. Suitable markers for NMR and ESR include those with a detectable characteristic spin, such as deuterium, which may be incorporated into the antibody by labeling of nutrients for the relevant hybridoma.

A protein-specific antibody or antibody fragment which has been labeled with
25 an appropriate detectable imaging moiety, such as a radioisotope (for example, ^{131}I , ^{112}In , $^{99\text{m}}\text{Tc}$), a radio-opaque substance, or a material detectable by nuclear magnetic resonance, is introduced (for example, parenterally, subcutaneously, or intraperitoneally) into the mammal. It will be understood in the art that the size of the subject and the imaging system used will determine the quantity of imaging moiety
30 needed to produce diagnostic images. In the case of a radioisotope moiety, for a human subject, the quantity of radioactivity injected will normally range from about 5 to 20 millicuries of $^{99\text{m}}\text{Tc}$. The labeled antibody or antibody fragment will then preferentially accumulate at the location of cells which contain the specific protein. In vivo tumor imaging is described in S.W. Burchiel et al., "Immunopharmacokinetics of
35 Radiolabeled Antibodies and Their Fragments." (Chapter 13 in Tumor Imaging: The Radiochemical Detection of Cancer, S.W. Burchiel and B. A. Rhodes, eds., Masson Publishing Inc. (1982).)

Thus, the invention provides a diagnostic method of a disorder, which involves (a) assaying the expression of a polypeptide of the present invention in cells or body fluid of an individual; (b) comparing the level of gene expression with a standard gene expression level, whereby an increase or decrease in the assayed polypeptide gene expression level compared to the standard expression level is indicative of a disorder.

Moreover, polypeptides of the present invention can be used to treat disease. For example, patients can be administered a polypeptide of the present invention in an effort to replace absent or decreased levels of the polypeptide (e.g., insulin), to supplement absent or decreased levels of a different polypeptide (e.g., hemoglobin S for hemoglobin B), to inhibit the activity of a polypeptide (e.g., an oncogene), to activate the activity of a polypeptide (e.g., by binding to a receptor), to reduce the activity of a membrane bound receptor by competing with it for free ligand (e.g., soluble TNF receptors used in reducing inflammation), or to bring about a desired response (e.g., blood vessel growth).

Similarly, antibodies directed to a polypeptide of the present invention can also be used to treat disease. For example, administration of an antibody directed to a polypeptide of the present invention can bind and reduce overproduction of the polypeptide. Similarly, administration of an antibody can activate the polypeptide, such as by binding to a polypeptide bound to a membrane (receptor).

At the very least, the polypeptides of the present invention can be used as molecular weight markers on SDS-PAGE gels or on molecular sieve gel filtration columns using methods well known to those of skill in the art. Polypeptides can also be used to raise antibodies, which in turn are used to measure protein expression from a recombinant cell, as a way of assessing transformation of the host cell. Moreover, the polypeptides of the present invention can be used to test the following biological activities.

Biological Activities

The polynucleotides and polypeptides of the present invention can be used in assays to test for one or more biological activities. If these polynucleotides and polypeptides do exhibit activity in a particular assay, it is likely that these molecules may be involved in the diseases associated with the biological activity. Thus, the polynucleotides and polypeptides could be used to treat the associated disease.

Immune Activity

A polypeptide or polynucleotide of the present invention may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the

proliferation, differentiation, or mobilization (chemotaxis) of immune cells. Immune cells develop through a process called hematopoiesis, producing myeloid (platelets, red blood cells, neutrophils, and macrophages) and lymphoid (B and T lymphocytes) cells from pluripotent stem cells. The etiology of these immune deficiencies or disorders
5 may be genetic, somatic, such as cancer or some autoimmune disorders, acquired (e.g., by chemotherapy or toxins), or infectious. Moreover, a polynucleotide or polypeptide of the present invention can be used as a marker or detector of a particular immune system disease or disorder.

A polynucleotide or polypeptide of the present invention may be useful in
10 treating or detecting deficiencies or disorders of hematopoietic cells. A polypeptide or polynucleotide of the present invention could be used to increase differentiation and proliferation of hematopoietic cells, including the pluripotent stem cells, in an effort to treat those disorders associated with a decrease in certain (or many) types hematopoietic cells. Examples of immunologic deficiency syndromes include, but are not limited to:
15 blood protein disorders (e.g. agammaglobulinemia, dysgammaglobulinemia), ataxia telangiectasia, common variable immunodeficiency, Digeorge Syndrome, HIV infection, HTLV-BLV infection, leukocyte adhesion deficiency syndrome, lymphopenia, phagocyte bactericidal dysfunction, severe combined immunodeficiency (SCIDs), Wiskott-Aldrich Disorder, anemia, thrombocytopenia, or hemoglobinuria.

Moreover, a polypeptide or polynucleotide of the present invention could also
20 be used to modulate hemostatic (the stopping of bleeding) or thrombolytic activity (clot formation). For example, by increasing hemostatic or thrombolytic activity, a polynucleotide or polypeptide of the present invention could be used to treat blood coagulation disorders (e.g., afibrinogenemia, factor deficiencies), blood platelet
25 disorders (e.g. thrombocytopenia), or wounds resulting from trauma, surgery, or other causes. Alternatively, a polynucleotide or polypeptide of the present invention that can decrease hemostatic or thrombolytic activity could be used to inhibit or dissolve clotting. These molecules could be important in the treatment of heart attacks (infarction), strokes, or scarring.

A polynucleotide or polypeptide of the present invention may also be useful in
30 treating or detecting autoimmune disorders. Many autoimmune disorders result from inappropriate recognition of self as foreign material by immune cells. This inappropriate recognition results in an immune response leading to the destruction of the host tissue. Therefore, the administration of a polypeptide or polynucleotide of the
35 present invention that inhibits an immune response, particularly the proliferation, differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing autoimmune disorders.

Examples of autoimmune disorders that can be treated or detected by the present invention include, but are not limited to: Addison's Disease, hemolytic anemia, antiphospholipid syndrome, rheumatoid arthritis, dermatitis, allergic encephalomyelitis, glomerulonephritis, Goodpasture's Syndrome, Graves' Disease, Multiple Sclerosis, Myasthenia Gravis, Neuritis, Ophthalmia, Bullous Pemphigoid, Pemphigus, Polyendocrinopathies, Purpura, Reiter's Disease, Stiff-Man Syndrome, Autoimmune Thyroiditis, Systemic Lupus Erythematosus, Autoimmune Pulmonary Inflammation, Guillain-Barre Syndrome, insulin dependent diabetes mellitus, and autoimmune inflammatory eye disease.

- 10 Similarly, allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems, may also be treated by a polypeptide or polynucleotide of the present invention. Moreover, these molecules can be used to treat anaphylaxis, hypersensitivity to an antigenic molecule, or blood group incompatibility.

- 15 A polynucleotide or polypeptide of the present invention may also be used to treat and/or prevent organ rejection or graft-versus-host disease (GVHD). Organ rejection occurs by host immune cell destruction of the transplanted tissue through an immune response. Similarly, an immune response is also involved in GVHD, but, in this case, the foreign transplanted immune cells destroy the host tissues. The administration of a polypeptide or polynucleotide of the present invention that inhibits an immune response, particularly the proliferation, differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing organ rejection or GVHD.

- 20 Similarly, a polypeptide or polynucleotide of the present invention may also be used to modulate inflammation. For example, the polypeptide or polynucleotide may inhibit the proliferation and differentiation of cells involved in an inflammatory response. These molecules can be used to treat inflammatory conditions, both chronic and acute conditions, including inflammation associated with infection (e.g., septic shock, sepsis, or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel disease, Crohn's disease, or resulting from over production of cytokines (e.g., TNF or IL-1.)

Hyperproliferative Disorders

- 35 A polypeptide or polynucleotide can be used to treat or detect hyperproliferative disorders, including neoplasms. A polypeptide or polynucleotide of the present invention may inhibit the proliferation of the disorder through direct or indirect

interactions. Alternatively, a polypeptide or polynucleotide of the present invention may proliferate other cells which can inhibit the hyperproliferative disorder.

For example, by increasing an immune response, particularly increasing antigenic qualities of the hyperproliferative disorder or by proliferating, differentiating, or mobilizing T-cells, hyperproliferative disorders can be treated. This immune response may be increased by either enhancing an existing immune response, or by initiating a new immune response. Alternatively, decreasing an immune response may also be a method of treating hyperproliferative disorders, such as a chemotherapeutic agent.

Examples of hyperproliferative disorders that can be treated or detected by a polynucleotide or polypeptide of the present invention include, but are not limited to neoplasms located in the: abdomen, bone, breast, digestive system, liver, pancreas, peritoneum, endocrine glands (adrenal, parathyroid, pituitary, testicles, ovary, thymus, thyroid), eye, head and neck, nervous (central and peripheral), lymphatic system, pelvic, skin, soft tissue, spleen, thoracic, and urogenital.

Similarly, other hyperproliferative disorders can also be treated or detected by a polynucleotide or polypeptide of the present invention. Examples of such hyperproliferative disorders include, but are not limited to: hypergammaglobulinemia, lymphoproliferative disorders, paraproteinemias, purpura, sarcoidosis, Sezary Syndrome, Waldenstrom's Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other hyperproliferative disease, besides neoplasia, located in an organ system listed above.

Infectious Disease

A polypeptide or polynucleotide of the present invention can be used to treat or detect infectious agents. For example, by increasing the immune response, particularly increasing the proliferation and differentiation of B and/or T cells, infectious diseases may be treated. The immune response may be increased by either enhancing an existing immune response, or by initiating a new immune response. Alternatively, the polypeptide or polynucleotide of the present invention may also directly inhibit the infectious agent, without necessarily eliciting an immune response.

Viruses are one example of an infectious agent that can cause disease or symptoms that can be treated or detected by a polynucleotide or polypeptide of the present invention. Examples of viruses, include, but are not limited to the following DNA and RNA viral families: Arbovirus, Adenoviridae, Arenaviridae, Arterivirus, Birnaviridae, Bunyaviridae, Caliciviridae, Circoviridae, Coronaviridae, Flaviviridae, Hepadnaviridae (Hepatitis), Herpesviridae (such as, Cytomegalovirus, Herpes

Simplex, Herpes Zoster), Mononegavirus (e.g., Paramyxoviridae, Morbillivirus, Rhabdoviridae), Orthomyxoviridae (e.g., Influenza), Papovaviridae, Parvoviridae, Picornaviridae, Poxviridae (such as Smallpox or Vaccinia), Reoviridae (e.g., Rotavirus), Retroviridae (HTLV-I, HTLV-II, Lentivirus), and Togaviridae (e.g., Rubivirus). Viruses falling within these families can cause a variety of diseases or symptoms, including, but not limited to: arthritis, bronchiolitis, encephalitis, eye infections (e.g., conjunctivitis, keratitis), chronic fatigue syndrome, hepatitis (A, B, C, E, Chronic Active, Delta), meningitis, opportunistic infections (e.g., AIDS), pneumonia, Burkitt's Lymphoma, chickenpox, hemorrhagic fever, Measles, Mumps, Parainfluenza, Rabies, the common cold, Polio, leukemia, Rubella, sexually transmitted diseases, skin diseases (e.g., Kaposi's, warts), and viremia. A polypeptide or polynucleotide of the present invention can be used to treat or detect any of these symptoms or diseases.

Similarly, bacterial or fungal agents that can cause disease or symptoms and that can be treated or detected by a polynucleotide or polypeptide of the present invention include, but not limited to, the following Gram-Negative and Gram-positive bacterial families and fungi: Actinomycetales (e.g., Corynebacterium, Mycobacterium, Norcardia), Aspergillosis, Bacillaceae (e.g., Anthrax, Clostridium), Bacteroidaceae, Blastomycosis, Bordetella, Borrelia, Brucellosis, Candidiasis, Campylobacter, Coccidioidomycosis, Cryptococcosis, Dermatocycoses, Enterobacteriaceae (Klebsiella, Salmonella, Serratia, Yersinia), Erysipelothrix, Helicobacter, Legionellosis, Leptospirosis, Listeria, Mycoplasmatales, Neisseriaceae (e.g., Acinetobacter, Gonorrhea, Meningococcal), Pasteurellaceae Infections (e.g., Actinobacillus, Haemophilus, Pasteurella), Pseudomonas, Rickettsiaceae, Chlamydiaceae, Syphilis, and Staphylococcal. These bacterial or fungal families can cause the following diseases or symptoms, including, but not limited to: bacteremia, endocarditis, eye infections (conjunctivitis, tuberculosis, uveitis), gingivitis, opportunistic infections (e.g., AIDS related infections), paronychia, prosthesis-related infections, Reiter's Disease, respiratory tract infections, such as Whooping Cough or Empyema, sepsis, Lyme Disease, Cat-Scratch Disease, Dysentery, Paratyphoid Fever, food poisoning, Typhoid, pneumonia, Gonorrhea, meningitis, Chlamydia, Syphilis, Diphtheria, Leprosy, Paratuberculosis, Tuberculosis, Lupus, Botulism, gangrene, tetanus, impetigo, Rheumatic Fever, Scarlet Fever, sexually transmitted diseases, skin diseases (e.g., cellulitis, dermatocycoses), toxemia, urinary tract infections, wound infections. A polypeptide or polynucleotide of the present invention can be used to treat or detect any of these symptoms or diseases.

Moreover, parasitic agents causing disease or symptoms that can be treated or detected by a polynucleotide or polypeptide of the present invention include, but not limited to, the following families: Amebiasis, Babesiosis, Coccidiosis, Cryptosporidiosis, Dientamoebiasis, Dourine, Ectoparasitic, Giardiasis, Helminthiasis, Leishmaniasis, Theileriasis, Toxoplasmosis, Trypanosomiasis, and Trichomonas. These parasites can cause a variety of diseases or symptoms, including, but not limited to: Scabies, Trombiculiasis, eye infections, intestinal disease (e.g., dysentery, giardiasis), liver disease, lung disease, opportunistic infections (e.g., AIDS related), Malaria, pregnancy complications, and toxoplasmosis. A polypeptide or polynucleotide of the present invention can be used to treat or detect any of these symptoms or diseases.

Preferably, treatment using a polypeptide or polynucleotide of the present invention could either be by administering an effective amount of a polypeptide to the patient, or by removing cells from the patient, supplying the cells with a polynucleotide of the present invention, and returning the engineered cells to the patient (ex vivo therapy). Moreover, the polypeptide or polynucleotide of the present invention can be used as an antigen in a vaccine to raise an immune response against infectious disease.

Regeneration

A polynucleotide or polypeptide of the present invention can be used to differentiate, proliferate, and attract cells, leading to the regeneration of tissues. (See. Science 276:59-87 (1997).) The regeneration of tissues could be used to repair, replace, or protect tissue damaged by congenital defects, trauma (wounds, burns, incisions, or ulcers), age, disease (e.g. osteoporosis, osteoarthritis, periodontal disease, liver failure), surgery, including cosmetic plastic surgery, fibrosis, reperfusion injury, or systemic cytokine damage.

Tissues that could be regenerated using the present invention include organs (e.g., pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac), vascular (including vascular endothelium), nervous, hematopoietic, and skeletal (bone, cartilage, tendon, and ligament) tissue. Preferably, regeneration occurs without or decreased scarring. Regeneration also may include angiogenesis.

Moreover, a polynucleotide or polypeptide of the present invention may increase regeneration of tissues difficult to heal. For example, increased tendon/ligament regeneration would quicken recovery time after damage. A polynucleotide or polypeptide of the present invention could also be used prophylactically in an effort to avoid damage. Specific diseases that could be treated include of tendinitis, carpal tunnel syndrome, and other tendon or ligament defects. A further example of tissue

regeneration of non-healing wounds includes pressure ulcers, ulcers associated with vascular insufficiency, surgical, and traumatic wounds.

Similarly, nerve and brain tissue could also be regenerated by using a polynucleotide or polypeptide of the present invention to proliferate and differentiate nerve cells. Diseases that could be treated using this method include central and peripheral nervous system diseases, neuropathies, or mechanical and traumatic disorders (e.g., spinal cord disorders, head trauma, cerebrovascular disease, and stroke). Specifically, diseases associated with peripheral nerve injuries, peripheral neuropathy (e.g., resulting from chemotherapy or other medical therapies), localized neuropathies, and central nervous system diseases (e.g., Alzheimer's disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome), could all be treated using the polynucleotide or polypeptide of the present invention.

15 Chemotaxis

A polynucleotide or polypeptide of the present invention may have chemotaxis activity. A chemotactic molecule attracts or mobilizes cells (e.g., monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells) to a particular site in the body, such as inflammation, infection, or site of hyperproliferation. The mobilized cells can then fight off and/or heal the particular trauma or abnormality.

A polynucleotide or polypeptide of the present invention may increase chemotactic activity of particular cells. These chemotactic molecules can then be used to treat inflammation, infection, hyperproliferative disorders, or any immune system disorder by increasing the number of cells targeted to a particular location in the body. For example, chemotactic molecules can be used to treat wounds and other trauma to tissues by attracting immune cells to the injured location. Chemotactic molecules of the present invention can also attract fibroblasts, which can be used to treat wounds.

It is also contemplated that a polynucleotide or polypeptide of the present invention may inhibit chemotactic activity. These molecules could also be used to treat disorders. Thus, a polynucleotide or polypeptide of the present invention could be used as an inhibitor of chemotaxis.

Binding Activity

A polypeptide of the present invention may be used to screen for molecules that bind to the polypeptide or for molecules to which the polypeptide binds. The binding of the polypeptide and the molecule may activate (agonist), increase, inhibit

(antagonist), or decrease activity of the polypeptide or the molecule bound. Examples of such molecules include antibodies, oligonucleotides, proteins (e.g., receptors), or small molecules.

Preferably, the molecule is closely related to the natural ligand of the polypeptide, e.g., a fragment of the ligand, or a natural substrate, a ligand, a structural or functional mimetic. (See, Coligan et al., Current Protocols in Immunology 1(2):Chapter 5 (1991).) Similarly, the molecule can be closely related to the natural receptor to which the polypeptide binds, or at least, a fragment of the receptor capable of being bound by the polypeptide (e.g., active site). In either case, the molecule can be rationally designed using known techniques.

Preferably, the screening for these molecules involves producing appropriate cells which express the polypeptide, either as a secreted protein or on the cell membrane. Preferred cells include cells from mammals, yeast, *Drosophila*, or *E. coli*. Cells expressing the polypeptide (or cell membrane containing the expressed polypeptide) are then preferably contacted with a test compound potentially containing the molecule to observe binding, stimulation, or inhibition of activity of either the polypeptide or the molecule.

The assay may simply test binding of a candidate compound to the polypeptide, wherein binding is detected by a label, or in an assay involving competition with a labeled competitor. Further, the assay may test whether the candidate compound results in a signal generated by binding to the polypeptide.

Alternatively, the assay can be carried out using cell-free preparations, polypeptide/molecule affixed to a solid support, chemical libraries, or natural product mixtures. The assay may also simply comprise the steps of mixing a candidate compound with a solution containing a polypeptide, measuring polypeptide/molecule activity or binding, and comparing the polypeptide/molecule activity or binding to a standard.

Preferably, an ELISA assay can measure polypeptide level or activity in a sample (e.g., biological sample) using a monoclonal or polyclonal antibody. The antibody can measure polypeptide level or activity by either binding, directly or indirectly, to the polypeptide or by competing with the polypeptide for a substrate.

All of these above assays can be used as diagnostic or prognostic markers. The molecules discovered using these assays can be used to treat disease or to bring about a particular result in a patient (e.g., blood vessel growth) by activating or inhibiting the polypeptide/molecule. Moreover, the assays can discover agents which may inhibit or enhance the production of the polypeptide from suitably manipulated cells or tissues.

Therefore, the invention includes a method of identifying compounds which bind to a polypeptide of the invention comprising the steps of: (a) incubating a candidate binding compound with a polypeptide of the invention; and (b) determining if binding has occurred. Moreover, the invention includes a method of identifying
5 agonists/antagonists comprising the steps of: (a) incubating a candidate compound with a polypeptide of the invention, (b) assaying a biological activity, and (b) determining if a biological activity of the polypeptide has been altered.

Other Activities

10 A polypeptide or polynucleotide of the present invention may also increase or decrease the differentiation or proliferation of embryonic stem cells, besides, as discussed above, hematopoietic lineage.

A polypeptide or polynucleotide of the present invention may also be used to modulate mammalian characteristics, such as body height, weight, hair color, eye color,
15 skin, percentage of adipose tissue, pigmentation, size, and shape (e.g., cosmetic surgery). Similarly, a polypeptide or polynucleotide of the present invention may be used to modulate mammalian metabolism affecting catabolism, anabolism, processing, utilization, and storage of energy.

A polypeptide or polynucleotide of the present invention may be used to change
20 a mammal's mental state or physical state by influencing biorhythms, cardiac rhythms, depression (including depressive disorders), tendency for violence, tolerance for pain, reproductive capabilities (preferably by Activin or Inhibin-like activity), hormonal or endocrine levels, appetite, libido, memory, stress, or other cognitive qualities.

25 A polypeptide or polynucleotide of the present invention may also be used as a food additive or preservative, such as to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components.

Other Preferred Embodiments

Other preferred embodiments of the claimed invention include an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 50 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1.

35 Also preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of

positions beginning with the nucleotide at about the position of the 5' Nucleotide of the Clone Sequence and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Also preferred is a nucleic acid molecule wherein said sequence of contiguous
5 nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the Start Codon and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Similarly preferred is a nucleic acid molecule wherein said sequence of
10 contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the First Amino Acid of the Signal Peptide and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide
15 sequence which is at least 95% identical to a sequence of at least about 150 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X.

Further preferred is an isolated nucleic acid molecule comprising a nucleotide
sequence which is at least 95% identical to a sequence of at least about 500 contiguous
20 nucleotides in the nucleotide sequence of SEQ ID NO:X.

A further preferred embodiment is a nucleic acid molecule comprising a
nucleotide sequence which is at least 95% identical to the nucleotide sequence of SEQ
ID NO:X beginning with the nucleotide at about the position of the 5' Nucleotide of the
First Amino Acid of the Signal Peptide and ending with the nucleotide at about the
25 position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in
Table 1.

A further preferred embodiment is an isolated nucleic acid molecule comprising
a nucleotide sequence which is at least 95% identical to the complete nucleotide
sequence of SEQ ID NO:X.

Also preferred is an isolated nucleic acid molecule which hybridizes under
30 stringent hybridization conditions to a nucleic acid molecule, wherein said nucleic acid molecule which hybridizes does not hybridize under stringent hybridization conditions to a nucleic acid molecule having a nucleotide sequence consisting of only A residues or of only T residues.

Also preferred is a composition of matter comprising a DNA molecule which
35 comprises a human cDNA clone identified by a cDNA Clone Identifier in Table 1, which DNA molecule is contained in the material deposited with the American Type

Culture Collection and given the ATCC Deposit Number shown in Table 1 for said cDNA Clone Identifier.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in the nucleotide sequence of a human cDNA clone identified by a cDNA Clone Identifier in Table 1, which DNA molecule is contained in the deposit given the ATCC Deposit Number shown in Table 1.

Also preferred is an isolated nucleic acid molecule, wherein said sequence of at least 50 contiguous nucleotides is included in the nucleotide sequence of the complete open reading frame sequence encoded by said human cDNA clone.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to sequence of at least 150 contiguous nucleotides in the nucleotide sequence encoded by said human cDNA clone.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to sequence of at least 500 contiguous nucleotides in the nucleotide sequence encoded by said human cDNA clone.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the complete nucleotide sequence encoded by said human cDNA clone.

A further preferred embodiment is a method for detecting in a biological sample a nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1; which method comprises a step of comparing a nucleotide sequence of at least one nucleic acid molecule in said sample with a sequence selected from said group and determining whether the sequence of said nucleic acid molecule in said sample is at least 95% identical to said selected sequence.

Also preferred is the above method wherein said step of comparing sequences comprises determining the extent of nucleic acid hybridization between nucleic acid molecules in said sample and a nucleic acid molecule comprising said sequence selected from said group. Similarly, also preferred is the above method wherein said step of comparing sequences is performed by comparing the nucleotide sequence determined from a nucleic acid molecule in said sample with said sequence selected from said group. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

A further preferred embodiment is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting nucleic acid molecules in said sample, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

The method for identifying the species, tissue or cell type of a biological sample can comprise a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a gene encoding a secreted protein identified in Table 1, which method comprises a step of detecting in a biological sample obtained from said subject nucleic acid molecules, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

The method for diagnosing a pathological condition can comprise a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

Also preferred is a composition of matter comprising isolated nucleic acid molecules wherein the nucleotide sequences of said nucleic acid molecules comprise a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1.

Also preferred is a polypeptide, wherein said sequence of contiguous amino acids is included in the amino acid sequence of SEQ ID NO:Y in the range of positions beginning with the residue at about the position of the First Amino Acid of the Secreted Portion and ending with the residue at about the Last Amino Acid of the Open Reading Frame as set forth for SEQ ID NO:Y in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 30 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to the complete amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is a polypeptide wherein said sequence of contiguous amino acids is included in the amino acid sequence of a secreted portion of the secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 30 contiguous amino acids in the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Further preferred is an isolated antibody which binds specifically to a polypeptide comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Further preferred is a method for detecting in a biological sample a polypeptide comprising an amino acid sequence which is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1; which method comprises a step of comparing an amino acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group and determining whether the sequence of said polypeptide molecule in said sample is at least 90% identical to said sequence of at least 10 contiguous amino acids.

Also preferred is the above method wherein said step of comparing an amino acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group comprises determining the extent of specific binding of polypeptides in said sample to an antibody which binds specifically to a polypeptide comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is the above method wherein said step of comparing sequences is performed by comparing the amino acid sequence determined from a polypeptide molecule in said sample with said sequence selected from said group.

Also preferred is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting polypeptide molecules in said sample, if any, comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is the above method for identifying the species, tissue or cell type of a biological sample, which method comprises a step of detecting polypeptide molecules comprising an amino acid sequence in a panel of at least two amino acid sequences, wherein at least one sequence in said panel is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the above group.

Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a gene encoding a secreted protein identified in Table 1, which method comprises a step of detecting in a biological sample obtained from said subject polypeptide molecules comprising an amino acid sequence in a panel of at least two amino acid sequences, wherein at least one sequence in said panel is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

In any of these methods, the step of detecting said polypeptide molecules includes using an antibody.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a nucleotide sequence encoding a polypeptide wherein said polypeptide comprises an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated nucleic acid molecule, wherein said nucleotide sequence encoding a polypeptide has been optimized for expression of said polypeptide in a prokaryotic host.

Also preferred is an isolated nucleic acid molecule, wherein said polypeptide
5 comprises an amino acid sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

10 Further preferred is a method of making a recombinant vector comprising inserting any of the above isolated nucleic acid molecule into a vector. Also preferred is the recombinant vector produced by this method. Also preferred is a method of making a recombinant host cell comprising introducing the vector into a host cell, as well as the recombinant host cell produced by this method.

15 Also preferred is a method of making an isolated polypeptide comprising culturing this recombinant host cell under conditions such that said polypeptide is expressed and recovering said polypeptide. Also preferred is this method of making an isolated polypeptide, wherein said recombinant host cell is a eukaryotic cell and said polypeptide is a secreted portion of a human secreted protein comprising an amino acid
20 sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y beginning with the residue at the position of the First Amino Acid of the Secreted Portion of SEQ ID NO:Y wherein Y is an integer set forth in Table 1 and said position of the First Amino Acid of the Secreted Portion of SEQ ID NO:Y is defined in Table 1; and an amino acid sequence of a secreted portion of a protein encoded by a human
25 cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1. The isolated polypeptide produced by this method is also preferred.

Also preferred is a method of treatment of an individual in need of an increased level of a secreted protein activity, which method comprises administering to such an
30 individual a pharmaceutical composition comprising an amount of an isolated polypeptide, polynucleotide, or antibody of the claimed invention effective to increase the level of said protein activity in said individual.

Having generally described the invention, the same will be more readily understood by reference to the following examples, which are provided by way of
35 illustration and are not intended as limiting.

Examples

Example 1: Isolation of a Selected cDNA Clone From the Deposited Sample

5 Each cDNA clone in a cited ATCC deposit is contained in a plasmid vector. Table 1 identifies the vectors used to construct the cDNA library from which each clone was isolated. In many cases, the vector used to construct the library is a phage vector from which a plasmid has been excised. The table immediately below correlates the related plasmid for each phage vector used in constructing the cDNA library. For
10 example, where a particular clone is identified in Table 1 as being isolated in the vector "Lambda Zap," the corresponding deposited clone is in "pBluescript."

	<u>Vector Used to Construct Library</u>	<u>Corresponding Deposited Plasmid</u>
	Lambda Zap	pBluescript (pBS)
	Uni-Zap XR	pBluescript (pBS)
15	Zap Express	pBK
	lafmid BA	plafmid BA
	pSport1	pSport1
	pCMVSPORT 2.0	pCMVSPORT 2.0
	pCMVSPORT 3.0	pCMVSPORT 3.0
20	pCR [®] 2.1	pCR [®] 2.1

Vectors Lambda Zap (U.S. Patent Nos. 5,128,256 and 5,286,636), Uni-Zap XR (U.S. Patent Nos. 5,128, 256 and 5,286,636), Zap Express (U.S. Patent Nos. 5,128,256 and 5,286,636), pBluescript (pBS) (Short, J. M. et al., Nucleic Acids Res. 16:7583-7600 (1988); Altling-Mees, M. A. and Short, J. M., Nucleic Acids Res. 25 17:9494 (1989)) and pBK (Altling-Mees, M. A. et al., Strategies 5:58-61 (1992)) are commercially available from Stratagene Cloning Systems, Inc., 11011 N. Torrey Pines Road, La Jolla, CA, 92037. pBS contains an ampicillin resistance gene and pBK contains a neomycin resistance gene. Both can be transformed into E. coli strain XL-1 Blue, also available from Stratagene. pBS comes in 4 forms SK+, SK-, KS+ and KS. The S and K refers to the orientation of the polylinker to the T7 and T3 primer
30 sequences which flank the polylinker region ("S" is for SacI and "K" is for KpnI which are the first sites on each respective end of the linker). "+" or "-" refer to the orientation of the f1 origin of replication ("ori"), such that in one orientation, single stranded rescue initiated from the f1 ori generates sense strand DNA and in the other, antisense.

35 Vectors pSport1, pCMVSPORT 2.0 and pCMVSPORT 3.0, were obtained from Life Technologies, Inc., P. O. Box 6009, Gaithersburg, MD 20897. All Sport vectors contain an ampicillin resistance gene and may be transformed into E. coli strain

DH10B, also available from Life Technologies. (See, for instance, Gruber, C. E., et al., Focus 15:59 (1993).) Vector lafmid BA (Bento Soares, Columbia University, NY) contains an ampicillin resistance gene and can be transformed into E. coli strain XL-1 Blue. Vector pCR[®]2.1, which is available from Invitrogen, 1600 Faraday Avenue,
5 Carlsbad, CA 92008, contains an ampicillin resistance gene and may be transformed into E. coli strain DH10B, available from Life Technologies. (See, for instance, Clark, J. M., Nuc. Acids Res. 16:9677-9686 (1988) and Mead, D. et al., Bio/Technology 9: (1991).) Preferably, a polynucleotide of the present invention does not comprise the phage vector sequences identified for the particular clone in Table 1, as well as the
10 corresponding plasmid vector sequences designated above.

The deposited material in the sample assigned the ATCC Deposit Number cited in Table 1 for any given cDNA clone also may contain one or more additional plasmids, each comprising a cDNA clone different from that given clone. Thus, deposits sharing the same ATCC Deposit Number contain at least a plasmid for each cDNA clone
15 identified in Table 1. Typically, each ATCC deposit sample cited in Table 1 comprises a mixture of approximately equal amounts (by weight) of about 50 plasmid DNAs, each containing a different cDNA clone; but such a deposit sample may include plasmids for more or less than 50 cDNA clones, up to about 500 cDNA clones.

Two approaches can be used to isolate a particular clone from the deposited
20 sample of plasmid DNAs cited for that clone in Table 1. First, a plasmid is directly isolated by screening the clones using a polynucleotide probe corresponding to SEQ ID NO:X.

Particularly, a specific polynucleotide with 30-40 nucleotides is synthesized using an Applied Biosystems DNA synthesizer according to the sequence reported.
25 The oligonucleotide is labeled, for instance, with ³²P-γ-ATP using T4 polynucleotide kinase and purified according to routine methods. (E.g., Maniatis et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, Cold Spring, NY (1982).) The plasmid mixture is transformed into a suitable host, as indicated above (such as XL-1 Blue (Stratagene)) using techniques known to those of skill in the art, such as
30 those provided by the vector supplier or in related publications or patents cited above. The transformants are plated on 1.5% agar plates (containing the appropriate selection agent, e.g., ampicillin) to a density of about 150 transformants (colonies) per plate. These plates are screened using Nylon membranes according to routine methods for bacterial colony screening (e.g., Sambrook et al., Molecular Cloning: A Laboratory
35 Manual, 2nd Edit., (1989), Cold Spring Harbor Laboratory Press, pages 1.93 to 1.104), or other techniques known to those of skill in the art.

Alternatively, two primers of 17-20 nucleotides derived from both ends of the SEQ ID NO:X (i.e., within the region of SEQ ID NO:X bounded by the 5' NT and the 3' NT of the clone defined in Table 1) are synthesized and used to amplify the desired cDNA using the deposited cDNA plasmid as a template. The polymerase chain reaction is carried out under routine conditions, for instance, in 25 μ l of reaction mixture with 0.5 μ g of the above cDNA template. A convenient reaction mixture is 1.5-5 mM $MgCl_2$, 0.01% (w/v) gelatin, 20 μ M each of dATP, dCTP, dGTP, dTTP, 25 pmol of each primer and 0.25 Unit of Taq polymerase. Thirty five cycles of PCR (denaturation at 94°C for 1 min; annealing at 55°C for 1 min; elongation at 72°C for 1 min) are performed with a Perkin-Elmer Cetus automated thermal cycler. The amplified product is analyzed by agarose gel electrophoresis and the DNA band with expected molecular weight is excised and purified. The PCR product is verified to be the selected sequence by subcloning and sequencing the DNA product.

Several methods are available for the identification of the 5' or 3' non-coding portions of a gene which may not be present in the deposited clone. These methods include but are not limited to, filter probing, clone enrichment using specific probes, and protocols similar or identical to 5' and 3' "RACE" protocols which are well known in the art. For instance, a method similar to 5' RACE is available for generating the missing 5' end of a desired full-length transcript. (Fromont-Racine et al., *Nucleic Acids Res.* 21(7):1683-1684 (1993).)

Briefly, a specific RNA oligonucleotide is ligated to the 5' ends of a population of RNA presumably containing full-length gene RNA transcripts. A primer set containing a primer specific to the ligated RNA oligonucleotide and a primer specific to a known sequence of the gene of interest is used to PCR amplify the 5' portion of the desired full-length gene. This amplified product may then be sequenced and used to generate the full length gene.

This above method starts with total RNA isolated from the desired source, although poly-A+ RNA can be used. The RNA preparation can then be treated with phosphatase if necessary to eliminate 5' phosphate groups on degraded or damaged RNA which may interfere with the later RNA ligase step. The phosphatase should then be inactivated and the RNA treated with tobacco acid pyrophosphatase in order to remove the cap structure present at the 5' ends of messenger RNAs. This reaction leaves a 5' phosphate group at the 5' end of the cap cleaved RNA which can then be ligated to an RNA oligonucleotide using T4 RNA ligase.

This modified RNA preparation is used as a template for first strand cDNA synthesis using a gene specific oligonucleotide. The first strand synthesis reaction is

used as a template for PCR amplification of the desired 5' end using a primer specific to the ligated RNA oligonucleotide and a primer specific to the known sequence of the gene of interest. The resultant product is then sequenced and analyzed to confirm that the 5' end sequence belongs to the desired gene.

5

Example 2: Isolation of Genomic Clones Corresponding to a Polynucleotide

A human genomic P1 library (Genomic Systems, Inc.) is screened by PCR using primers selected for the cDNA sequence corresponding to SEQ ID NO:X., according to the method described in Example 1. (See also, Sambrook.)

10

Example 3: Tissue Distribution of Polypeptide

Tissue distribution of mRNA expression of polynucleotides of the present invention is determined using protocols for Northern blot analysis, described by, among others, Sambrook et al. For example, a cDNA probe produced by the method described in Example 1 is labeled with P³² using the rediprime™ DNA labeling system (Amersham Life Science), according to manufacturer's instructions. After labeling, the probe is purified using CHROMA SPIN-100™ column (Clontech Laboratories, Inc.), according to manufacturer's protocol number PT1200-1. The purified labeled probe is then used to examine various human tissues for mRNA expression.

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Multiple Tissue Northern (MTN) blots containing various human tissues (H) or human immune system tissues (IM) (Clontech) are examined with the labeled probe using ExpressHyb™ hybridization solution (Clontech) according to manufacturer's protocol number PT1190-1. Following hybridization and washing, the blots are mounted and exposed to film at -70°C overnight, and the films developed according to standard procedures.

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Example 4: Chromosomal Mapping of the Polynucleotides

An oligonucleotide primer set is designed according to the sequence at the 5' end of SEQ ID NO:X. This primer preferably spans about 100 nucleotides. This primer set is then used in a polymerase chain reaction under the following set of conditions : 30 seconds, 95°C; 1 minute, 56°C; 1 minute, 70°C. This cycle is repeated 32 times followed by one 5 minute cycle at 70°C. Human, mouse, and hamster DNA is used as template in addition to a somatic cell hybrid panel containing individual chromosomes or chromosome fragments (Bios, Inc). The reactions is analyzed on

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either 8% polyacrylamide gels or 3.5 % agarose gels. Chromosome mapping is determined by the presence of an approximately 100 bp PCR fragment in the particular somatic cell hybrid.

5 **Example 5: Bacterial Expression of a Polypeptide**

A polynucleotide encoding a polypeptide of the present invention is amplified using PCR oligonucleotide primers corresponding to the 5' and 3' ends of the DNA sequence, as outlined in Example 1, to synthesize insertion fragments. The primers used to amplify the cDNA insert should preferably contain restriction sites, such as
10 BamHI and XbaI, at the 5' end of the primers in order to clone the amplified product into the expression vector. For example, BamHI and XbaI correspond to the restriction enzyme sites on the bacterial expression vector pQE-9. (Qiagen, Inc., Chatsworth, CA). This plasmid vector encodes antibiotic resistance (Amp^r), a bacterial origin of replication (ori), an IPTG-regulatable promoter/operator (P/O), a ribosome binding site
15 (RBS), a 6-histidine tag (6-His), and restriction enzyme cloning sites.

The pQE-9 vector is digested with BamHI and XbaI and the amplified fragment is ligated into the pQE-9 vector maintaining the reading frame initiated at the bacterial RBS. The ligation mixture is then used to transform the E. coli strain M15/rep4 (Qiagen, Inc.) which contains multiple copies of the plasmid pREP4, which expresses
20 the lacI repressor and also confers kanamycin resistance (Kan^r). Transformants are identified by their ability to grow on LB plates and ampicillin/kanamycin resistant colonies are selected. Plasmid DNA is isolated and confirmed by restriction analysis.

Clones containing the desired constructs are grown overnight (O/N) in liquid culture in LB media supplemented with both Amp (100 ug/ml) and Kan (25 ug/ml).
25 The O/N culture is used to inoculate a large culture at a ratio of 1:100 to 1:250. The cells are grown to an optical density 600 (O.D.⁶⁰⁰) of between 0.4 and 0.6. IPTG (Isopropyl-B-D-thiogalacto pyranoside) is then added to a final concentration of 1 mM. IPTG induces by inactivating the lacI repressor, clearing the P/O leading to increased gene expression.

30 Cells are grown for an extra 3 to 4 hours. Cells are then harvested by centrifugation (20 mins at 6000Xg). The cell pellet is solubilized in the chaotropic agent 6 Molar Guanidine HCl by stirring for 3-4 hours at 4°C. The cell debris is removed by centrifugation, and the supernatant containing the polypeptide is loaded onto a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (available from
35 QIAGEN, Inc., *supra*). Proteins with a 6 x His tag bind to the Ni-NTA resin with high

affinity and can be purified in a simple one-step procedure (for details see: The QIAexpressionist (1995) QIAGEN, Inc., *supra*).

Briefly, the supernatant is loaded onto the column in 6 M guanidine-HCl, pH 8, the column is first washed with 10 volumes of 6 M guanidine-HCl, pH 8, then washed
5 with 10 volumes of 6 M guanidine-HCl pH 6, and finally the polypeptide is eluted with 6 M guanidine-HCl, pH 5.

The purified protein is then renatured by dialyzing it against phosphate-buffered saline (PBS) or 50 mM Na-acetate, pH 6 buffer plus 200 mM NaCl. Alternatively, the protein can be successfully refolded while immobilized on the Ni-NTA column. The
10 recommended conditions are as follows: renature using a linear 6M-1M urea gradient in 500 mM NaCl, 20% glycerol, 20 mM Tris/HCl pH 7.4, containing protease inhibitors. The renaturation should be performed over a period of 1.5 hours or more. After renaturation the proteins are eluted by the addition of 250 mM imidazole. Imidazole is removed by a final dialyzing step against PBS or 50 mM sodium acetate pH 6 buffer
15 plus 200 mM NaCl. The purified protein is stored at 4°C or frozen at -80°C.

In addition to the above expression vector, the present invention further includes an expression vector comprising phage operator and promoter elements operatively linked to a polynucleotide of the present invention, called pHE4a. (ATCC Accession Number 209645, deposited on February 25, 1998.) This vector contains: 1) a
20 neomycinphosphotransferase gene as a selection marker, 2) an E. coli origin of replication, 3) a T5 phage promoter sequence, 4) two lac operator sequences, 5) a Shine-Delgarno sequence, and 6) the lactose operon repressor gene (*lacIq*). The origin of replication (*oriC*) is derived from pUC19 (LTI, Gaithersburg, MD). The promoter sequence and operator sequences are made synthetically.

DNA can be inserted into the pHEa by restricting the vector with NdeI and
25 XbaI, BamHI, XhoI, or Asp718, running the restricted product on a gel, and isolating the larger fragment (the stuffer fragment should be about 310 base pairs). The DNA insert is generated according to the PCR protocol described in Example 1, using PCR primers having restriction sites for NdeI (5' primer) and XbaI, BamHI, XhoI, or
30 Asp718 (3' primer). The PCR insert is gel purified and restricted with compatible enzymes. The insert and vector are ligated according to standard protocols.

The engineered vector could easily be substituted in the above protocol to express protein in a bacterial system.

35 Example 6: Purification of a Polypeptide from an Inclusion Body

The following alternative method can be used to purify a polypeptide expressed in *E. coli* when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10°C.

Upon completion of the production phase of the *E. coli* fermentation, the cell
5 culture is cooled to 4-10°C and the cells harvested by continuous centrifugation at 15,000 rpm (Heraeus Sepatech). On the basis of the expected yield of protein per unit weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a
10 high shear mixer.

The cells are then lysed by passing the solution through a microfluidizer (Microfluidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by centrifugation at 7000 xg for 15 min. The resultant pellet is washed again using 0.5M
15 NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 xg centrifugation for 15 min., the pellet is discarded and the polypeptide containing supernatant is incubated at 4°C overnight to allow further GuHCl extraction.

20 Following high speed centrifugation (30,000 xg) to remove insoluble particles, the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous stirring. The refolded diluted protein solution is kept at 4°C without mixing for 12 hours prior to further purification steps.

25 To clarify the refolded polypeptide solution, a previously prepared tangential filtration unit equipped with 0.16 µm membrane filter with appropriate surface area (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive Biosystems). The column is washed with 40 mM sodium acetate, pH 6.0 and eluted
30 with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same buffer, in a stepwise manner. The absorbance at 280 nm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

Fractions containing the polypeptide are then pooled and mixed with 4 volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem

columns of strong anion (Poros HQ-50, Perseptive Biosystems) and weak anion (Poros CM-20, Perseptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column
5 volume linear gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5. Fractions are collected under constant A_{280} monitoring of the effluent. Fractions containing the polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant polypeptide should exhibit greater than 95% purity after the above
10 refolding and purification steps. No major contaminant bands should be observed from Commaassie blue stained 16% SDS-PAGE gel when 5 μ g of purified protein is loaded. The purified protein can also be tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

15 Example 7: Cloning and Expression of a Polypeptide in a Baculovirus Expression System

In this example, the plasmid shuttle vector pA2 is used to insert a polynucleotide into a baculovirus to express a polypeptide. This expression vector contains the strong polyhedrin promoter of the *Autographa californica* nuclear polyhedrosis virus
20 (AcMNPV) followed by convenient restriction sites such as BamHI, Xba I and Asp718. The polyadenylation site of the simian virus 40 ("SV40") is used for efficient polyadenylation. For easy selection of recombinant virus, the plasmid contains the beta-galactosidase gene from *E. coli* under control of a weak *Drosophila* promoter in the same orientation, followed by the polyadenylation signal of the polyhedrin gene. The
25 inserted genes are flanked on both sides by viral sequences for cell-mediated homologous recombination with wild-type viral DNA to generate a viable virus that express the cloned polynucleotide.

Many other baculovirus vectors can be used in place of the vector above, such as pAc373, pVL941, and pAcIM1, as one skilled in the art would readily appreciate, as
30 long as the construct provides appropriately located signals for transcription, translation, secretion and the like, including a signal peptide and an in-frame AUG as required. Such vectors are described, for instance, in Luckow et al., *Virology* 170:31-39 (1989).

Specifically, the cDNA sequence contained in the deposited clone, including the
35 AUG initiation codon and the naturally associated leader sequence identified in Table 1, is amplified using the PCR protocol described in Example 1. If the naturally occurring

signal sequence is used to produce the secreted protein, the pA2 vector does not need a second signal peptide. Alternatively, the vector can be modified (pA2 GP) to include a baculovirus leader sequence, using the standard methods described in Summers et al., "A Manual of Methods for Baculovirus Vectors and Insect Cell Culture Procedures,"

- 5 Texas Agricultural Experimental Station Bulletin No. 1555 (1987).

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("GeneClean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

- 10 The plasmid is digested with the corresponding restriction enzymes and optionally, can be dephosphorylated using calf intestinal phosphatase, using routine procedures known in the art. The DNA is then isolated from a 1% agarose gel using a commercially available kit ("GeneClean" BIO 101 Inc., La Jolla, Ca.).

- 15 The fragment and the dephosphorylated plasmid are ligated together with T4 DNA ligase. *E. coli* HB101 or other suitable *E. coli* hosts such as XL-1 Blue (Stratagene Cloning Systems, La Jolla, CA) cells are transformed with the ligation mixture and spread on culture plates. Bacteria containing the plasmid are identified by digesting DNA from individual colonies and analyzing the digestion product by gel electrophoresis. The sequence of the cloned fragment is confirmed by DNA sequencing.

- 20 Five µg of a plasmid containing the polynucleotide is co-transfected with 1.0 µg of a commercially available linearized baculovirus DNA ("BaculoGold™ baculovirus DNA", Pharmingen, San Diego, CA), using the lipofection method described by Felgner et al., Proc. Natl. Acad. Sci. USA 84:7413-7417 (1987). One µg of BaculoGold™ virus DNA and 5 µg of the plasmid are mixed in a sterile well of a
25 microtiter plate containing 50 µl of serum-free Grace's medium (Life Technologies Inc., Gaithersburg, MD). Afterwards, 10 µl Lipofectin plus 90 µl Grace's medium are added, mixed and incubated for 15 minutes at room temperature. Then the transfection mixture is added drop-wise to Sf9 insect cells (ATCC CRL 1711) seeded in a 35 mm
30 incubated for 5 hours at 27° C. The transfection solution is then removed from the plate and 1 ml of Grace's insect medium supplemented with 10% fetal calf serum is added. Cultivation is then continued at 27° C for four days.

- After four days the supernatant is collected and a plaque assay is performed, as described by Summers and Smith, *supra*. An agarose gel with "Blue Gal" (Life
35 Technologies Inc., Gaithersburg) is used to allow easy identification and isolation of gal-expressing clones, which produce blue-stained plaques. (A detailed description of a "plaque assay" of this type can also be found in the user's guide for insect cell culture

and baculovirology distributed by Life Technologies Inc., Gaithersburg, page 9-10.) After appropriate incubation, blue stained plaques are picked with the tip of a micropipettor (e.g., Eppendorf). The agar containing the recombinant viruses is then resuspended in a microcentrifuge tube containing 200 µl of Grace's medium and the suspension containing the recombinant baculovirus is used to infect Sf9 cells seeded in 35 mm dishes. Four days later the supernatants of these culture dishes are harvested and then they are stored at 4° C.

To verify the expression of the polypeptide, Sf9 cells are grown in Grace's medium supplemented with 10% heat-inactivated FBS. The cells are infected with the recombinant baculovirus containing the polynucleotide at a multiplicity of infection ("MOI") of about 2. If radiolabeled proteins are desired, 6 hours later the medium is removed and is replaced with SF900 II medium minus methionine and cysteine (available from Life Technologies Inc., Rockville, MD). After 42 hours, 5 µCi of ³⁵S-methionine and 5 µCi ³⁵S-cysteine (available from Amersham) are added. The cells are further incubated for 16 hours and then are harvested by centrifugation. The proteins in the supernatant as well as the intracellular proteins are analyzed by SDS-PAGE followed by autoradiography (if radiolabeled).

Microsequencing of the amino acid sequence of the amino terminus of purified protein may be used to determine the amino terminal sequence of the produced protein.

Example 8: Expression of a Polypeptide in Mammalian Cells

The polypeptide of the present invention can be expressed in a mammalian cell. A typical mammalian expression vector contains a promoter element, which mediates the initiation of transcription of mRNA, a protein coding sequence, and signals required for the termination of transcription and polyadenylation of the transcript. Additional elements include enhancers, Kozak sequences and intervening sequences flanked by donor and acceptor sites for RNA splicing. Highly efficient transcription is achieved with the early and late promoters from SV40, the long terminal repeats (LTRs) from Retroviruses, e.g., RSV, HTLVI, HIVI and the early promoter of the cytomegalovirus (CMV). However, cellular elements can also be used (e.g., the human actin promoter).

Suitable expression vectors for use in practicing the present invention include, for example, vectors such as pSVL and pMSG (Pharmacia, Uppsala, Sweden), pRSVcat (ATCC 37152), pSV2dhfr (ATCC 37146), pBC12MI (ATCC 67109), pCMVSPORT 2.0, and pCMVSPORT 3.0. Mammalian host cells that could be used include, human Hela, 293, H9 and Jurkat cells, mouse NIH3T3 and C127 cells, Cos 1, Cos 7 and CV1, quail QC1-3 cells, mouse L cells and Chinese hamster ovary (CHO) cells.

Alternatively, the polypeptide can be expressed in stable cell lines containing the polynucleotide integrated into a chromosome. The co-transfection with a selectable marker such as dhfr, gpt, neomycin, hygromycin allows the identification and isolation of the transfected cells.

5 The transfected gene can also be amplified to express large amounts of the encoded protein. The DHFR (dihydrofolate reductase) marker is useful in developing cell lines that carry several hundred or even several thousand copies of the gene of interest. (See, e.g., Alt, F. W., et al., J. Biol. Chem. 253:1357-1370 (1978); Hamlin, J. L. and Ma, C., Biochem. et Biophys. Acta, 1097:107-143 (1990); Page, M. J. and
10 Sydenham, M. A., Biotechnology 9:64-68 (1991).) Another useful selection marker is the enzyme glutamine synthase (GS) (Murphy et al., Biochem J. 227:277-279 (1991); Bebbington et al., Bio/Technology 10:169-175 (1992). Using these markers, the mammalian cells are grown in selective medium and the cells with the highest resistance are selected. These cell lines contain the amplified gene(s) integrated into a
15 chromosome. Chinese hamster ovary (CHO) and NSO cells are often used for the production of proteins.

Derivatives of the plasmid pSV2-dhfr (ATCC Accession No. 37146), the expression vectors pC4 (ATCC Accession No. 209646) and pC6 (ATCC Accession No. 209647) contain the strong promoter (LTR) of the Rous Sarcoma Virus (Cullen et al., Molecular and Cellular Biology, 438-447 (March, 1985)) plus a fragment of the
20 CMV-enhancer (Boshart et al., Cell 41:521-530 (1985).) Multiple cloning sites, e.g., with the restriction enzyme cleavage sites BamHI, XbaI and Asp718, facilitate the cloning of the gene of interest. The vectors also contain the 3' intron, the polyadenylation and termination signal of the rat preproinsulin gene, and the mouse
25 DHFR gene under control of the SV40 early promoter.

Specifically, the plasmid pC6, for example, is digested with appropriate restriction enzymes and then dephosphorylated using calf intestinal phosphates by procedures known in the art. The vector is then isolated from a 1% agarose gel.

30 A polynucleotide of the present invention is amplified according to the protocol outlined in Example 1. If the naturally occurring signal sequence is used to produce the secreted protein, the vector does not need a second signal peptide. Alternatively, if the naturally occurring signal sequence is not used, the vector can be modified to include a heterologous signal sequence. (See, e.g., WO 96/34891.)

35 The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("GeneClean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

The amplified fragment is then digested with the same restriction enzyme and purified on a 1% agarose gel. The isolated fragment and the dephosphorylated vector are then ligated with T4 DNA ligase. *E. coli* HB101 or XL-1 Blue cells are then transformed and bacteria are identified that contain the fragment inserted into plasmid pC6 using, for instance, restriction enzyme analysis.

Chinese hamster ovary cells lacking an active DHFR gene is used for transfection. Five µg of the expression plasmid pC6 is cotransfected with 0.5 µg of the plasmid pSVneo using lipofectin (Felgner et al., *supra*). The plasmid pSV2-neo contains a dominant selectable marker, the *neo* gene from Tn5 encoding an enzyme that confers resistance to a group of antibiotics including G418. The cells are seeded in alpha minus MEM supplemented with 1 mg/ml G418. After 2 days, the cells are trypsinized and seeded in hybridoma cloning plates (Greiner, Germany) in alpha minus MEM supplemented with 10, 25, or 50 ng/ml of methotrexate plus 1 mg/ml G418. After about 10-14 days single clones are trypsinized and then seeded in 6-well petri dishes or 10 ml flasks using different concentrations of methotrexate (50 nM, 100 nM, 200 nM, 400 nM, 800 nM). Clones growing at the highest concentrations of methotrexate are then transferred to new 6-well plates containing even higher concentrations of methotrexate (1 µM, 2 µM, 5 µM, 10 mM, 20 mM). The same procedure is repeated until clones are obtained which grow at a concentration of 100 - 200 µM. Expression of the desired gene product is analyzed, for instance, by SDS-PAGE and Western blot or by reversed phase HPLC analysis.

Example 9: Protein Fusions

The polypeptides of the present invention are preferably fused to other proteins. These fusion proteins can be used for a variety of applications. For example, fusion of the present polypeptides to His-tag, HA-tag, protein A, IgG domains, and maltose binding protein facilitates purification. (See Example 5; see also EP A 394,827; Traunecker, et al., Nature 331:84-86 (1988).) Similarly, fusion to IgG-1, IgG-3, and albumin increases the halflife time in vivo. Nuclear localization signals fused to the polypeptides of the present invention can target the protein to a specific subcellular localization, while covalent heterodimer or homodimers can increase or decrease the activity of a fusion protein. Fusion proteins can also create chimeric molecules having more than one function. Finally, fusion proteins can increase solubility and/or stability of the fused protein compared to the non-fused protein. All of the types of fusion proteins described above can be made by modifying the following protocol, which outlines the fusion of a polypeptide to an IgG molecule, or the protocol described in Example 5.

Briefly, the human Fc portion of the IgG molecule can be PCR amplified, using primers that span the 5' and 3' ends of the sequence described below. These primers also should have convenient restriction enzyme sites that will facilitate cloning into an expression vector, preferably a mammalian expression vector.

- 5 For example, if pC4 (Accession No. 209646) is used, the human Fc portion can be ligated into the BamHI cloning site. Note that the 3' BamHI site should be destroyed. Next, the vector containing the human Fc portion is re-restricted with BamHI, linearizing the vector, and a polynucleotide of the present invention, isolated by the PCR protocol described in Example 1, is ligated into this BamHI site. Note that
10 the polynucleotide is cloned without a stop codon, otherwise a fusion protein will not be produced.

- If the naturally occurring signal sequence is used to produce the secreted protein, pC4 does not need a second signal peptide. Alternatively, if the naturally occurring signal sequence is not used, the vector can be modified to include a
15 heterologous signal sequence. (See, e.g., WO 96/34891.)

Human IgG Fc region:

- GGGATCCGGAGCCCAAATCTTCTGACAAACTCACACATGCCCACCGTGCC
CAGCACCTGAATTCGAGGGTGACCGTCAGTCTTCTCTTCCCCCAAACCC
20 CAAGGACACCCTCATGATCTCCCGGACTCCTGAGGTCACATGCGTGTTGGT
GGACGTAAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACG
GCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAAC
AGCACGTACCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTG
AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAACCCCC
25 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGT
GTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCT
GACCTGCCTGGTCAAAGGCTTCTATCCAAGCGACATCGCCGTGGAGTGGGA
GAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCTGG
ACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCA
30 GGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGC
ACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGAGTGC
GACGGCCGCGACTCTAGAGGAT (SEQ ID NO:1)

Example 10: Production of an Antibody from a Polypeptide

- 35 The antibodies of the present invention can be prepared by a variety of methods. (See, Current Protocols, Chapter 2.) For example, cells expressing a polypeptide of the present invention is administered to an animal to induce the production of sera

containing polyclonal antibodies. In a preferred method, a preparation of the secreted protein is prepared and purified to render it substantially free of natural contaminants. Such a preparation is then introduced into an animal in order to produce polyclonal antisera of greater specific activity.

5 In the most preferred method, the antibodies of the present invention are monoclonal antibodies (or protein binding fragments thereof). Such monoclonal antibodies can be prepared using hybridoma technology. (Köhler et al., *Nature* 256:495 (1975); Köhler et al., *Eur. J. Immunol.* 6:511 (1976); Köhler et al., *Eur. J. Immunol.* 6:292 (1976); Hammerling et al., in: *Monoclonal Antibodies and T-Cell*
10 *Hybridomas*, Elsevier, N.Y., pp. 563-681 (1981).) In general, such procedures involve immunizing an animal (preferably a mouse) with polypeptide or, more preferably, with a secreted polypeptide-expressing cell. Such cells may be cultured in any suitable tissue culture medium; however, it is preferable to culture cells in Earle's modified Eagle's medium supplemented with 10% fetal bovine serum (inactivated at
15 about 56°C), and supplemented with about 10 g/l of nonessential amino acids, about 1,000 U/ml of penicillin, and about 100 µg/ml of streptomycin.

The splenocytes of such mice are extracted and fused with a suitable myeloma cell line. Any suitable myeloma cell line may be employed in accordance with the present invention; however, it is preferable to employ the parent myeloma cell line
20 (SP2O), available from the ATCC. After fusion, the resulting hybridoma cells are selectively maintained in HAT medium, and then cloned by limiting dilution as described by Wands et al. (*Gastroenterology* 80:225-232 (1981).) The hybridoma cells obtained through such a selection are then assayed to identify clones which secrete antibodies capable of binding the polypeptide.

25 Alternatively, additional antibodies capable of binding to the polypeptide can be produced in a two-step procedure using anti-idiotypic antibodies. Such a method makes use of the fact that antibodies are themselves antigens, and therefore, it is possible to obtain an antibody which binds to a second antibody. In accordance with this method, protein specific antibodies are used to immunize an animal, preferably a
30 mouse. The splenocytes of such an animal are then used to produce hybridoma cells, and the hybridoma cells are screened to identify clones which produce an antibody whose ability to bind to the protein-specific antibody can be blocked by the polypeptide. Such antibodies comprise anti-idiotypic antibodies to the protein-specific antibody and can be used to immunize an animal to induce formation of further protein-specific
35 antibodies.

It will be appreciated that Fab and F(ab')₂ and other fragments of the antibodies of the present invention may be used according to the methods disclosed herein. Such fragments are typically produced by proteolytic cleavage, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')₂ fragments). Alternatively, secreted protein-binding fragments can be produced through the application of recombinant DNA technology or through synthetic chemistry.

For in vivo use of antibodies in humans, it may be preferable to use "humanized" chimeric monoclonal antibodies. Such antibodies can be produced using genetic constructs derived from hybridoma cells producing the monoclonal antibodies described above. Methods for producing chimeric antibodies are known in the art. (See, for review, Morrison, Science 229:1202 (1985); Oi et al., BioTechniques 4:214 (1986); Cabilly et al., U.S. Patent No. 4,816,567; Taniguchi et al., EP 171496; Morrison et al., EP 173494; Neuberger et al., WO 8601533; Robinson et al., WO 8702671; Boulianne et al., Nature 312:643 (1984); Neuberger et al., Nature 314:268 (1985).)

Example 11: Production Of Secreted Protein For High-Throughput Screening Assays

The following protocol produces a supernatant containing a polypeptide to be tested. This supernatant can then be used in the Screening Assays described in Examples 13-20.

First, dilute Poly-D-Lysine (644 587 Boehringer-Mannheim) stock solution (1mg/ml in PBS) 1:20 in PBS (w/o calcium or magnesium 17-516F Biowhittaker) for a working solution of 50ug/ml. Add 200 ul of this solution to each well (24 well plates) and incubate at RT for 20 minutes. Be sure to distribute the solution over each well (note: a 12-channel pipetter may be used with tips on every other channel). Aspirate off the Poly-D-Lysine solution and rinse with 1ml PBS (Phosphate Buffered Saline). The PBS should remain in the well until just prior to plating the cells and plates may be poly-lysine coated in advance for up to two weeks.

Plate 293T cells (do not carry cells past P+20) at 2×10^5 cells/well in .5ml DMEM(Dulbecco's Modified Eagle Medium)(with 4.5 G/L glucose and L-glutamine (12-604F Biowhittaker))/10% heat inactivated FBS(14-503F Biowhittaker)/1x Penstrep(17-602E Biowhittaker). Let the cells grow overnight.

The next day, mix together in a sterile solution basin: 300 ul Lipofectamine (18324-012 Gibco/BRL) and 5ml Optimem I (31985070 Gibco/BRL)/96-well plate. With a small volume multi-channel pipetter, aliquot approximately 2ug of an expression vector containing a polynucleotide insert, produced by the methods described in

Examples 8 or 9, into an appropriately labeled 96-well round bottom plate. With a multi-channel pipetter, add 50ul of the Lipofectamine/Optimem I mixture to each well. Pipette up and down gently to mix. Incubate at RT 15-45 minutes. After about 20 minutes, use a multi-channel pipetter to add 150ul Optimem I to each well. As a control, one plate of vector DNA lacking an insert should be transfected with each set of transfections.

Preferably, the transfection should be performed by tag-teaming the following tasks. By tag-teaming, hands on time is cut in half, and the cells do not spend too much time on PBS. First, person A aspirates off the media from four 24-well plates of cells, and then person B rinses each well with .5-1ml PBS. Person A then aspirates off PBS rinse, and person B, using a 12-channel pipetter with tips on every other channel, adds the 200ul of DNA/Lipofectamine/Optimem I complex to the odd wells first, then to the even wells. to each row on the 24-well plates. Incubate at 37°C for 6 hours.

While cells are incubating, prepare appropriate media, either 1%BSA in DMEM with 1x penstrep, or CHO-5 media (116.6 mg/L of CaCl₂ (anhyd); 0.00130 mg/L CuSO₄·5H₂O; 0.050 mg/L of Fe(NO₃)₃·9H₂O; 0.417 mg/L of FeSO₄·7H₂O; 311.80 mg/L of KCl; 28.64 mg/L of MgCl₂; 48.84 mg/L of MgSO₄; 6995.50 mg/L of NaCl; 2400.0 mg/L of NaHCO₃; 62.50 mg/L of NaH₂PO₄·H₂O; 71.02 mg/L of Na₂HPO₄; .4320 mg/L of ZnSO₄·7H₂O; .002 mg/L of Arachidonic Acid ; 1.022 mg/L of Cholesterol; .070 mg/L of DL-alpha-Tocopherol-Acetate; 0.0520 mg/L of Linoleic Acid; 0.010 mg/L of Linolenic Acid; 0.010 mg/L of Myristic Acid; 0.010 mg/L of Oleic Acid; 0.010 mg/L of Palmitic Acid; 0.010 mg/L of Palmitic Acid; 100 mg/L of Pluronic F-68; 0.010 mg/L of Stearic Acid; 2.20 mg/L of Tween 80; 4551 mg/L of D-Glucose; 130.85 mg/ml of L- Alanine; 147.50 mg/ml of L-Arginine-HCL; 7.50 mg/ml of L-Asparagine-H₂O; 6.65 mg/ml of L-Aspartic Acid; 29.56 mg/ml of L-Cystine-2HCL-H₂O; 31.29 mg/ml of L-Cystine-2HCL; 7.35 mg/ml of L-Glutamic Acid; 365.0 mg/ml of L-Glutamine; 18.75 mg/ml of Glycine; 52.48 mg/ml of L-Histidine-HCL-H₂O; 106.97 mg/ml of L-Isoleucine; 111.45 mg/ml of L-Leucine; 163.75 mg/ml of L-Lysine HCL; 32.34 mg/ml of L-Methionine; 68.48 mg/ml of L-Phenylalanine; 40.0 mg/ml of L-Proline; 26.25 mg/ml of L-Serine; 101.05 mg/ml of L-Threonine; 19.22 mg/ml of L-Tryptophan; 91.79 mg/ml of L-Tyrosine-2Na-2H₂O; 99.65 mg/ml of L-Valine; 0.0035 mg/L of Biotin; 3.24 mg/L of D-Ca Pantothenate; 11.78 mg/L of Choline Chloride; 4.65 mg/L of Folic Acid; 15.60 mg/L of i-Inositol; 3.02 mg/L of Niacinamide; 3.00 mg/L of Pyridoxal HCL; 0.031 mg/L of Pyridoxine HCL; 0.319 mg/L of Riboflavin; 3.17 mg/L of Thiamine HCL; 0.365 mg/L of Thymidine; and 0.680 mg/L of Vitamin B₁₂; 25 mM of HEPES Buffer; 2.39 mg/L of Na Hypoxanthine;

0.105 mg/L of Lipoic Acid; 0.081 mg/L of Sodium Putrescine-2HCL; 55.0 mg/L of Sodium Pyruvate; 0.0067 mg/L of Sodium Selenite; 20uM of Ethanolamine; 0.122 mg/L of Ferric Citrate; 41.70 mg/L of Methyl-B-Cyclodextrin complexed with Linoleic Acid; 33.33 mg/L of Methyl-B-Cyclodextrin complexed with Oleic Acid; and 10 mg/L of Methyl-B-Cyclodextrin complexed with Retinal) with 2mm glutamine and 1x pensrep. (BSA (81-068-3 Bayer) 100gm dissolved in 1L DMEM for a 10% BSA stock solution). Filter the media and collect 50 ul for endotoxin assay in 15ml polystyrene conical.

The transfection reaction is terminated, preferably by tag-teaming, at the end of the incubation period. Person A aspirates off the transfection media, while person B adds 1.5ml appropriate media to each well. Incubate at 37°C for 45 or 72 hours depending on the media used: 1%BSA for 45 hours or CHO-5 for 72 hours.

On day four, using a 300ul multichannel pipetter, aliquot 600ul in one 1ml deep well plate and the remaining supernatant into a 2ml deep well. The supernatants from each well can then be used in the assays described in Examples 13-20.

It is specifically understood that when activity is obtained in any of the assays described below using a supernatant, the activity originates from either the polypeptide directly (e.g., as a secreted protein) or by the polypeptide inducing expression of other proteins, which are then secreted into the supernatant. Thus, the invention further provides a method of identifying the protein in the supernatant characterized by an activity in a particular assay.

Example 12: Construction of GAS Reporter Construct

One signal transduction pathway involved in the differentiation and proliferation of cells is called the Jaks-STATs pathway. Activated proteins in the Jaks-STATs pathway bind to gamma activation site "GAS" elements or interferon-sensitive responsive element ("ISRE"), located in the promoter of many genes. The binding of a protein to these elements alter the expression of the associated gene.

GAS and ISRE elements are recognized by a class of transcription factors called Signal Transducers and Activators of Transcription, or "STATs." There are six members of the STATs family. Stat1 and Stat3 are present in many cell types, as is Stat2 (as response to IFN-alpha is widespread). Stat4 is more restricted and is not in many cell types though it has been found in T helper class I, cells after treatment with IL-12. Stat5 was originally called mammary growth factor, but has been found at higher concentrations in other cells including myeloid cells. It can be activated in tissue culture cells by many cytokines.

The STATs are activated to translocate from the cytoplasm to the nucleus upon tyrosine phosphorylation by a set of kinases known as the Janus Kinase ("Jaks") family. Jaks represent a distinct family of soluble tyrosine kinases and include Tyk2, Jak1, Jak2, and Jak3. These kinases display significant sequence similarity and are
5 generally catalytically inactive in resting cells.

The Jaks are activated by a wide range of receptors summarized in the Table below. (Adapted from review by Schidler and Darnell, Ann. Rev. Biochem. 64:621-51 (1995).) A cytokine receptor family, capable of activating Jaks, is divided into two
10 groups: (a) Class 1 includes receptors for IL-2, IL-3, IL-4, IL-6, IL-7, IL-9, IL-11, IL-12, IL-15, Epo, PRL, GH, G-CSF, GM-CSF, LIF, CNTF, and thrombopoietin; and (b) Class 2 includes IFN- α , IFN- γ , and IL-10. The Class 1 receptors share a conserved cysteine motif (a set of four conserved cysteines and one tryptophan) and a WSXWS motif (a membrane proximal region encoding Trp-Ser-Xxx-Trp-Ser (SEQ ID NO:2)).

15 Thus, on binding of a ligand to a receptor, Jaks are activated, which in turn activate STATs, which then translocate and bind to GAS elements. This entire process is encompassed in the Jaks-STATs signal transduction pathway.

Therefore, activation of the Jaks-STATs pathway, reflected by the binding of the GAS or the ISRE element, can be used to indicate proteins involved in the
20 proliferation and differentiation of cells. For example, growth factors and cytokines are known to activate the Jaks-STATs pathway. (See Table below.) Thus, by using GAS elements linked to reporter molecules, activators of the Jaks-STATs pathway can be identified.

	<u>Ligand</u>	<u>tyk2</u>	<u>JAKs</u> <u>Jak1</u>	<u>Jak2</u>	<u>Jak3</u>	<u>STATS</u>	<u>GAS(elements) or ISRE</u>
<u>IFN family</u>							
5	IFN- α /B	+	+	-	-	1,2,3	ISRE
	IFN-g		+	+	-	1	GAS (IRF1>Lys6>IFP)
	IL-10	+	?	?	-	1,3	
<u>gp130 family</u>							
10	IL-6 (Pleiotrohic)	+	+	+	?	1,3	GAS (IRF1>Lys6>IFP)
	IL-11(Pleiotrohic)	?	+	?	?	1,3	
	OnM(Pleiotrohic)	?	+	+	?	1,3	
	LIF(Pleiotrohic)	?	+	+	?	1,3	
	CNTF(Pleiotrohic)	-/+	+	+	?	1,3	
15	G-CSF(Pleiotrohic)	?	+	?	?	1,3	
	IL-12(Pleiotrohic)	+	-	+	+	1,3	
<u>g-C family</u>							
20	IL-2 (lymphocytes)	-	+	-	+	1,3,5	GAS
	IL-4 (lymph/myeloid)	-	+	-	+	6	GAS (IRF1 = IFP >>Ly6)(IgH)
	IL-7 (lymphocytes)	-	+	-	+	5	GAS
	IL-9 (lymphocytes)	-	+	-	+	5	GAS
	IL-13 (lymphocyte)	-	+	?	?	6	GAS
	IL-15	?	+	?	+	5	GAS
25							
<u>gp140 family</u>							
	IL-3 (myeloid)	-	-	+	-	5	GAS (IRF1>IFP>>Ly6)
	IL-5 (myeloid)	-	-	+	-	5	GAS
	GM-CSF (myeloid)	-	-	+	-	5	GAS
30							
<u>Growth hormone family</u>							
	GH	?	-	+	-	5	
	PRL	?	+/-	+	-	1,3,5	
	EPO	?	-	+	-	5	GAS(B-CAS>IRF1=IFP>>Ly6)
35							
<u>Receptor Tyrosine Kinases</u>							
	EGF	?	+	+	-	1,3	GAS (IRF1)
	PDGF	?	+	+	-	1,3	
	CSF-1	?	+	+	-	1,3	GAS (not IRF1)
40							

To construct a synthetic GAS containing promoter element, which is used in the Biological Assays described in Examples 13-14, a PCR based strategy is employed to generate a GAS-SV40 promoter sequence. The 5' primer contains four tandem copies of the GAS binding site found in the IRF1 promoter and previously demonstrated to bind STATs upon induction with a range of cytokines (Rothman et al., Immunity 1:457-468 (1994).), although other GAS or ISRE elements can be used instead. The 5' primer also contains 18bp of sequence complementary to the SV40 early promoter sequence and is flanked with an XhoI site. The sequence of the 5' primer is:
5':GCGCCTCGAGATTTCCCCGAAATCTAGATTTCCCCGAAATGATTTCCCCG
10 AAATGATTTCCCCGAAATATCTGCCATCTCAATTAG:3' (SEQ ID NO:3)

The downstream primer is complementary to the SV40 promoter and is flanked with a Hind III site: 5':GCGGCAAGCTTTTTGCAAAGCCTAGGC:3' (SEQ ID NO:4)

PCR amplification is performed using the SV40 promoter template present in the B-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is digested with XhoI/Hind III and subcloned into BLSK2-. (Stratagene.) Sequencing with forward and reverse primers confirms that the insert contains the following sequence:
5':CTCGAGATTTCCCCGAAATCTAGATTTCCCCGAAATGATTTCCCCGAAATG
20 ATTTCCCCGAAATATCTGCCATCTCAATTAGTCAGCAACCATAGTCCCGCCC
CTAACTCCGCCCATCCCGCCCCTAACTCCGCCAGTTCCGCCATTCTCCGC
CCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGC
CTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTT
TGCAAAAAGCTT:3' (SEQ ID NO:5)

25 With this GAS promoter element linked to the SV40 promoter, a GAS:SEAP2 reporter construct is next engineered. Here, the reporter molecule is a secreted alkaline phosphatase, or "SEAP." Clearly, however, any reporter molecule can be instead of SEAP, in this or in any of the other Examples. Well known reporter molecules that can be used instead of SEAP include chloramphenicol acetyltransferase (CAT), luciferase,
30 alkaline phosphatase, B-galactosidase, green fluorescent protein (GFP), or any protein detectable by an antibody.

The above sequence confirmed synthetic GAS-SV40 promoter element is subcloned into the pSEAP-Promoter vector obtained from Clontech using HindIII and XhoI, effectively replacing the SV40 promoter with the amplified GAS:SV40 promoter
35 element, to create the GAS-SEAP vector. However, this vector does not contain a neomycin resistance gene, and therefore, is not preferred for mammalian expression systems.

Thus, in order to generate mammalian stable cell lines expressing the GAS-SEAP reporter, the GAS-SEAP cassette is removed from the GAS-SEAP vector using SalI and NotI, and inserted into a backbone vector containing the neomycin resistance gene, such as pGFP-1 (Clontech), using these restriction sites in the multiple cloning site, to create the GAS-SEAP/Neo vector. Once this vector is transfected into mammalian cells, this vector can then be used as a reporter molecule for GAS binding as described in Examples 13-14.

Other constructs can be made using the above description and replacing GAS with a different promoter sequence. For example, construction of reporter molecules containing NFK-B and EGR promoter sequences are described in Examples 15 and 16. However, many other promoters can be substituted using the protocols described in these Examples. For instance, SRE, IL-2, NFAT, or Osteocalcin promoters can be substituted, alone or in combination (e.g., GAS/NF-KB/EGR, GAS/NF-KB, IL-2/NFAT, or NF-KB/GAS). Similarly, other cell lines can be used to test reporter construct activity, such as HELA (epithelial), HUVEC (endothelial), Reh (B-cell), Saos-2 (osteoblast), HUVAC (aortic), or Cardiomyocyte.

Example 13: High-Throughput Screening Assay for T-cell Activity.

The following protocol is used to assess T-cell activity by identifying factors, such as growth factors and cytokines, that may proliferate or differentiate T-cells. T-cell activity is assessed using the GAS/SEAP/Neo construct produced in Example 12. Thus, factors that increase SEAP activity indicate the ability to activate the Jaks-STATS signal transduction pathway. The T-cell used in this assay is Jurkat T-cells (ATCC Accession No. TIB-152), although Molt-3 cells (ATCC Accession No. CRL-1552) and Molt-4 cells (ATCC Accession No. CRL-1582) cells can also be used.

Jurkat T-cells are lymphoblastic CD4+ Th1 helper cells. In order to generate stable cell lines, approximately 2 million Jurkat cells are transfected with the GAS-SEAP/neo vector using DMRIE-C (Life Technologies)(transfection procedure described below). The transfected cells are seeded to a density of approximately 20,000 cells per well and transfectants resistant to 1 mg/ml gentamicin selected. Resistant colonies are expanded and then tested for their response to increasing concentrations of interferon gamma. The dose response of a selected clone is demonstrated.

Specifically, the following protocol will yield sufficient cells for 75 wells containing 200 ul of cells. Thus, it is either scaled up, or performed in multiple to generate sufficient cells for multiple 96 well plates. Jurkat cells are maintained in RPMI + 10% serum with 1%Pen-Strep. Combine 2.5 mls of OPTI-MEM (Life Technologies)

with 10 ug of plasmid DNA in a T25 flask. Add 2.5 ml OPTI-MEM containing 50 ul of DMRIE-C and incubate at room temperature for 15-45 mins.

During the incubation period, count cell concentration, spin down the required number of cells (10^7 per transfection), and resuspend in OPTI-MEM to a final
5 concentration of 10^7 cells/ml. Then add 1ml of 1×10^7 cells in OPTI-MEM to T25 flask and incubate at 37°C for 6 hrs. After the incubation, add 10 ml of RPMI + 15% serum.

The Jurkat:GAS-SEAP stable reporter lines are maintained in RPMI + 10% serum, 1 mg/ml Genticin, and 1% Pen-Strep. These cells are treated with supernatants containing a polypeptide as produced by the protocol described in Example 11.

10 On the day of treatment with the supernatant, the cells should be washed and resuspended in fresh RPMI + 10% serum to a density of 500,000 cells per ml. The exact number of cells required will depend on the number of supernatants being screened. For one 96 well plate, approximately 10 million cells (for 10 plates, 100 million cells) are required.

15 Transfer the cells to a triangular reservoir boat, in order to dispense the cells into a 96 well dish, using a 12 channel pipette. Using a 12 channel pipette, transfer 200 ul of cells into each well (therefore adding 100,000 cells per well).

After all the plates have been seeded, 50 ul of the supernatants are transferred directly from the 96 well plate containing the supernatants into each well using a 12
20 channel pipette. In addition, a dose of exogenous interferon gamma (0.1, 1.0, 10 ng) is added to wells H9, H10, and H11 to serve as additional positive controls for the assay.

The 96 well dishes containing Jurkat cells treated with supernatants are placed in an incubator for 48 hrs (note: this time is variable between 48-72 hrs). 35 ul samples
25 from each well are then transferred to an opaque 96 well plate using a 12 channel pipette. The opaque plates should be covered (using sellophene covers) and stored at -20°C until SEAP assays are performed according to Example 17. The plates containing the remaining treated cells are placed at 4°C and serve as a source of material for repeating the assay on a specific well if desired.

30 As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate Jurkat T cells. Over 30 fold induction is typically observed in the positive control wells.

35 **Example 14: High-Throughput Screening Assay Identifying Myeloid Activity**

The following protocol is used to assess myeloid activity by identifying factors, such as growth factors and cytokines, that may proliferate or differentiate myeloid cells. Myeloid cell activity is assessed using the GAS/SEAP/Neo construct produced in Example 12. Thus, factors that increase SEAP activity indicate the ability to activate the
5 Jaks-STATS signal transduction pathway. The myeloid cell used in this assay is U937, a pre-monocyte cell line, although TF-1, HL60, or KG1 can be used.

To transiently transfect U937 cells with the GAS/SEAP/Neo construct produced in Example 12, a DEAE-Dextran method (Kharbanda et. al., 1994, Cell Growth & Differentiation, 5:259-265) is used. First, harvest 2×10^7 U937 cells and wash with
10 PBS. The U937 cells are usually grown in RPMI 1640 medium containing 10% heat-inactivated fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 mg/ml streptomycin.

Next, suspend the cells in 1 ml of 20 mM Tris-HCl (pH 7.4) buffer containing 0.5 mg/ml DEAE-Dextran, 8 ug GAS-SEAP2 plasmid DNA, 140 mM NaCl, 5 mM
15 KCl, 375 uM $\text{Na}_2\text{HPO}_4 \cdot 7\text{H}_2\text{O}$, 1 mM MgCl_2 , and 675 uM CaCl_2 . Incubate at 37°C for 45 min.

Wash the cells with RPMI 1640 medium containing 10% FBS and then resuspend in 10 ml complete medium and incubate at 37°C for 36 hr.

The GAS-SEAP/U937 stable cells are obtained by growing the cells in 400
20 ug/ml G418. The G418-free medium is used for routine growth but every one to two months, the cells should be re-grown in 400 ug/ml G418 for couple of passages.

These cells are tested by harvesting 1×10^8 cells (this is enough for ten 96-well plates assay) and wash with PBS. Suspend the cells in 200 ml above described growth medium, with a final density of 5×10^5 cells/ml. Plate 200 ul cells per well in the 96-
25 well plate (or 1×10^5 cells/well).

Add 50 ul of the supernatant prepared by the protocol described in Example 11. Incubate at 37°C for 48 to 72 hr. As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate U937 cells. Over 30 fold induction is typically observed in the positive control wells. SEAP assay the supernatant according to the
30 protocol described in Example 17.

Example 15: High-Throughput Screening Assay Identifying Neuronal Activity.

When cells undergo differentiation and proliferation, a group of genes are
35 activated through many different signal transduction pathways. One of these genes, EGR1 (early growth response gene 1), is induced in various tissues and cell types upon

activation. The promoter of EGR1 is responsible for such induction. Using the EGR1 promoter linked to reporter molecules, activation of cells can be assessed.

Particularly, the following protocol is used to assess neuronal activity in PC12 cell lines. PC12 cells (rat phenochromocytoma cells) are known to proliferate and/or
5 differentiate by activation with a number of mitogens, such as TPA (tetradecanoyl phorbol acetate), NGF (nerve growth factor), and EGF (epidermal growth factor). The EGR1 gene expression is activated during this treatment. Thus, by stably transfecting PC12 cells with a construct containing an EGR promoter linked to SEAP reporter, activation of PC12 cells can be assessed.

10 The EGR/SEAP reporter construct can be assembled by the following protocol. The EGR-1 promoter sequence (-633 to +1)(Sakamoto K et al., Oncogene 6:867-871 (1991)) can be PCR amplified from human genomic DNA using the following primers:

5' GCGCTCGAGGGATGACAGCGATAGAACCCCGG -3' (SEQ ID NO:6)

5' GCGAAGCTTCGCGACTCCCGGATCCGCCTC-3' (SEQ ID NO:7)

15 Using the GAS:SEAP/Neo vector produced in Example 12, EGR1 amplified product can then be inserted into this vector. Linearize the GAS:SEAP/Neo vector using restriction enzymes XhoI/HindIII, removing the GAS/SV40 stuffer. Restrict the EGR1 amplified product with these same enzymes. Ligate the vector and the EGR1 promoter.

20 To prepare 96 well-plates for cell culture, two mls of a coating solution (1:30 dilution of collagen type I (Upstate Biotech Inc. Cat#08-115) in 30% ethanol (filter sterilized)) is added per one 10 cm plate or 50 ml per well of the 96-well plate, and allowed to air dry for 2 hr.

PC12 cells are routinely grown in RPMI-1640 medium (Bio Whittaker)
25 containing 10% horse serum (JRH BIOSCIENCES, Cat. # 12449-78P), 5% heat-inactivated fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 ug/ml streptomycin on a precoated 10 cm tissue culture dish. One to four split is done every three to four days. Cells are removed from the plates by scraping and resuspended with pipetting up and down for more than 15 times.

30 Transfect the EGR/SEAP/Neo construct into PC12 using the Lipofectamine protocol described in Example 11. EGR-SEAP/PC12 stable cells are obtained by growing the cells in 300 ug/ml G418. The G418-free medium is used for routine growth but every one to two months, the cells should be re-grown in 300 ug/ml G418 for couple of passages.

35 To assay for neuronal activity, a 10 cm plate with cells around 70 to 80% confluent is screened by removing the old medium. Wash the cells once with PBS

(Phosphate buffered saline). Then starve the cells in low serum medium (RPMI-1640 containing 1% horse serum and 0.5% FBS with antibiotics) overnight.

The next morning, remove the medium and wash the cells with PBS. Scrape off the cells from the plate, suspend the cells well in 2 ml low serum medium. Count
5 the cell number and add more low serum medium to reach final cell density as 5×10^5 cells/ml.

Add 200 μ l of the cell suspension to each well of 96-well plate (equivalent to 1×10^5 cells/well). Add 50 μ l supernatant produced by Example 11, 37°C for 48 to 72 hr. As a positive control, a growth factor known to activate PC12 cells through EGR
10 can be used, such as 50 ng/ μ l of Neuronal Growth Factor (NGF). Over fifty-fold induction of SEAP is typically seen in the positive control wells. SEAP assay the supernatant according to Example 17.

Example 16: High-Throughput Screening Assay for T-cell Activity

15 NF- κ B (Nuclear Factor κ B) is a transcription factor activated by a wide variety of agents including the inflammatory cytokines IL-1 and TNF, CD30 and CD40, lymphotoxin-alpha and lymphotoxin-beta, by exposure to LPS or thrombin, and by expression of certain viral gene products. As a transcription factor, NF- κ B regulates the expression of genes involved in immune cell activation, control of apoptosis (NF-
20 κ B appears to shield cells from apoptosis), B and T-cell development, anti-viral and antimicrobial responses, and multiple stress responses.

In non-stimulated conditions, NF- κ B is retained in the cytoplasm with I- κ B (Inhibitor κ B). However, upon stimulation, I- κ B is phosphorylated and degraded, causing NF- κ B to shuttle to the nucleus, thereby activating transcription of target
25 genes. Target genes activated by NF- κ B include IL-2, IL-6, GM-CSF, ICAM-1 and class 1 MHC.

Due to its central role and ability to respond to a range of stimuli, reporter constructs utilizing the NF- κ B promoter element are used to screen the supernatants produced in Example 11. Activators or inhibitors of NF- κ B would be useful in treating
30 diseases. For example, inhibitors of NF- κ B could be used to treat those diseases related to the acute or chronic activation of NF- κ B, such as rheumatoid arthritis.

To construct a vector containing the NF- κ B promoter element, a PCR based strategy is employed. The upstream primer contains four tandem copies of the NF- κ B binding site (GGGGACTTTCCC) (SEQ ID NO:8), 18 bp of sequence complementary to the 5' end of the SV40 early promoter sequence, and is flanked with an XhoI site:

5 5':GCGGCCTCGAGGGGACTTTCCCGGGGACTTTCCGGGGACTTTCCGGGAC
TTTCCATCCTGCCATCTCAATTAG:3' (SEQ ID NO:9)

The downstream primer is complementary to the 3' end of the SV40 promoter and is flanked with a Hind III site:

5':GCGGCAAGCTTTTTGCAAAGCCTAGGC:3' (SEQ ID NO:4)

10 PCR amplification is performed using the SV40 promoter template present in the pB-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is digested with XhoI and Hind III and subcloned into BLSK2-. (Stratagene) Sequencing with the T7 and T3 primers confirms the insert contains the following sequence:

15 5':CTCGAGGGGACTTTCCCGGGGACTTTCCGGGGACTTTCCGGGACTTTCC
ATCTGCCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCCA
TCCCGCCCCTAACTCCGCCCAGTTCGCCCCATTCTCCGCCCCATGGCTGACT
AATTTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTC
20 CAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCCTTTTGCAAAAAGCTT:
3' (SEQ ID NO:10)

Next, replace the SV40 minimal promoter element present in the pSEAP2- promoter plasmid (Clontech) with this NF- κ B/SV40 fragment using XhoI and HindIII.

25 However, this vector does not contain a neomycin resistance gene, and therefore, is not preferred for mammalian expression systems.

In order to generate stable mammalian cell lines, the NF- κ B/SV40/SEAP cassette is removed from the above NF- κ B/SEAP vector using restriction enzymes SalI and NotI, and inserted into a vector containing neomycin resistance. Particularly, the

30 NF- κ B/SV40/SEAP cassette was inserted into pGFP-1 (Clontech), replacing the GFP gene, after restricting pGFP-1 with SalI and NotI.

Once NF- κ B/SV40/SEAP/Neo vector is created, stable Jurkat T-cells are created and maintained according to the protocol described in Example 13. Similarly, the method for assaying supernatants with these stable Jurkat T-cells is also described

in Example 13. As a positive control, exogenous TNF alpha (0.1, 1, 10 ng) is added to wells H9, H10, and H11, with a 5-10 fold activation typically observed.

Example 17: Assay for SEAP Activity

- 5 As a reporter molecule for the assays described in Examples 13-16, SEAP activity is assayed using the Tropix Phospho-light Kit (Cat. BP-400) according to the following general procedure. The Tropix Phospho-light Kit supplies the Dilution, Assay, and Reaction Buffers used below.

- 10 Prime a dispenser with the 2.5x Dilution Buffer and dispense 15 µl of 2.5x dilution buffer into Optiplates containing 35 µl of a supernatant. Seal the plates with a plastic sealer and incubate at 65°C for 30 min. Separate the Optiplates to avoid uneven heating.

- Cool the samples to room temperature for 15 minutes. Empty the dispenser and prime with the Assay Buffer. Add 50 µl Assay Buffer and incubate at room temperature 5 min. Empty the dispenser and prime with the Reaction Buffer (see the table below). Add 50 µl Reaction Buffer and incubate at room temperature for 20 minutes. Since the intensity of the chemiluminescent signal is time dependent, and it takes about 10 minutes to read 5 plates on luminometer, one should treat 5 plates at each time and start the second set 10 minutes later.

- 20 Read the relative light unit in the luminometer. Set H12 as blank, and print the results. An increase in chemiluminescence indicates reporter activity.

Reaction Buffer Formulation:

# of plates	Rxn buffer diluent (ml)	CSPD (ml)
10	60	3
11	65	3.25
12	70	3.5
13	75	3.75
14	80	4
15	85	4.25
16	90	4.5
17	95	4.75
18	100	5
19	105	5.25
20	110	5.5
21	115	5.75
22	120	6
23	125	6.25
24	130	6.5
25	135	6.75
26	140	7
27	145	7.25

28	150	7.5
29	155	7.75
30	160	8
31	165	8.25
32	170	8.5
33	175	8.75
34	180	9
35	185	9.25
36	190	9.5
37	195	9.75
38	200	10
39	205	10.25
40	210	10.5
41	215	10.75
42	220	11
43	225	11.25
44	230	11.5
45	235	11.75
46	240	12
47	245	12.25
48	250	12.5
49	255	12.75
50	260	13

Example 18: High-Throughput Screening Assay Identifying Changes in Small Molecule Concentration and Membrane Permeability

Binding of a ligand to a receptor is known to alter intracellular levels of small molecules, such as calcium, potassium, sodium, and pH, as well as alter membrane potential. These alterations can be measured in an assay to identify supernatants which bind to receptors of a particular cell. Although the following protocol describes an assay for calcium, this protocol can easily be modified to detect changes in potassium, sodium, pH, membrane potential, or any other small molecule which is detectable by a fluorescent probe.

The following assay uses Fluorometric Imaging Plate Reader ("FLIPR") to measure changes in fluorescent molecules (Molecular Probes) that bind small molecules. Clearly, any fluorescent molecule detecting a small molecule can be used instead of the calcium fluorescent molecule, fluo-3, used here.

For adherent cells, seed the cells at 10,000 -20,000 cells/well in a Co-star black 96-well plate with clear bottom. The plate is incubated in a CO₂ incubator for 20 hours. The adherent cells are washed two times in Biotek washer with 200 ul of HBSS (Hank's Balanced Salt Solution) leaving 100 ul of buffer after the final wash.

A stock solution of 1 mg/ml fluo-3 is made in 10% pluronic acid DMSO. To load the cells with fluo-3, 50 ul of 12 ug/ml fluo-3 is added to each well. The plate is

incubated at 37°C in a CO₂ incubator for 60 min. The plate is washed four times in the Biotek washer with HBSS leaving 100 ul of buffer.

For non-adherent cells, the cells are spun down from culture media. Cells are re-suspended to 2-5x10⁶ cells/ml with HBSS in a 50-ml conical tube. 4 ul of 1 mg/ml fluo-3 solution in 10% pluronic acid DMSO is added to each ml of cell suspension. The tube is then placed in a 37°C water bath for 30-60 min. The cells are washed twice with HBSS, resuspended to 1x10⁶ cells/ml, and dispensed into a microplate, 100 ul/well. The plate is centrifuged at 1000 rpm for 5 min. The plate is then washed once in Denley CellWash with 200 ul, followed by an aspiration step to 100 ul final volume.

For a non-cell based assay, each well contains a fluorescent molecule, such as fluo-3. The supernatant is added to the well, and a change in fluorescence is detected.

To measure the fluorescence of intracellular calcium, the FLIPR is set for the following parameters: (1) System gain is 300-800 mW; (2) Exposure time is 0.4 second; (3) Camera F/stop is F/2; (4) Excitation is 488 nm; (5) Emission is 530 nm; and (6) Sample addition is 50 ul. Increased emission at 530 nm indicates an extracellular signaling event which has resulted in an increase in the intracellular Ca⁺⁺ concentration.

Example 19: High-Throughput Screening Assay Identifying Tyrosine Kinase Activity

The Protein Tyrosine Kinases (PTK) represent a diverse group of transmembrane and cytoplasmic kinases. Within the Receptor Protein Tyrosine Kinase (RPTK) group are receptors for a range of mitogenic and metabolic growth factors including the PDGF, FGF, EGF, NGF, HGF and Insulin receptor subfamilies. In addition there are a large family of RPTKs for which the corresponding ligand is unknown. Ligands for RPTKs include mainly secreted small proteins, but also membrane-bound and extracellular matrix proteins.

Activation of RPTK by ligands involves ligand-mediated receptor dimerization, resulting in transphosphorylation of the receptor subunits and activation of the cytoplasmic tyrosine kinases. The cytoplasmic tyrosine kinases include receptor associated tyrosine kinases of the src-family (e.g., src, yes, lck, lyn, fyn) and non-receptor linked and cytosolic protein tyrosine kinases, such as the Jak family, members of which mediate signal transduction triggered by the cytokine superfamily of receptors (e.g., the Interleukins, Interferons, GM-CSF, and Leptin).

Because of the wide range of known factors capable of stimulating tyrosine kinase activity, the identification of novel human secreted proteins capable of activating

tyrosine kinase signal transduction pathways are of interest. Therefore, the following protocol is designed to identify those novel human secreted proteins capable of activating the tyrosine kinase signal transduction pathways.

Seed target cells (e.g., primary keratinocytes) at a density of approximately
5 25,000 cells per well in a 96 well Loprodyne Silent Screen Plates purchased from
Nalge Nunc (Naperville, IL). The plates are sterilized with two 30 minute rinses with
100% ethanol, rinsed with water and dried overnight. Some plates are coated for 2 hr
with 100 ml of cell culture grade type I collagen (50 mg/ml), gelatin (2%) or polylysine
(50 mg/ml), all of which can be purchased from Sigma Chemicals (St. Louis, MO) or
10 10% Matrigel purchased from Becton Dickinson (Bedford, MA), or calf serum, rinsed
with PBS and stored at 4°C. Cell growth on these plates is assayed by seeding 5,000
cells/well in growth medium and indirect quantitation of cell number through use of
alarmarBlue as described by the manufacturer Alamar Biosciences, Inc. (Sacramento,
CA) after 48 hr. Falcon plate covers #3071 from Becton Dickinson (Bedford, MA) are
15 used to cover the Loprodyne Silent Screen Plates. Falcon Microtest III cell culture
plates can also be used in some proliferation experiments.

To prepare extracts, A431 cells are seeded onto the nylon membranes of
Loprodyne plates (20,000/200ml/well) and cultured overnight in complete medium.
Cells are quiesced by incubation in serum-free basal medium for 24 hr. After 5-20
20 minutes treatment with EGF (60ng/ml) or 50 ul of the supernatant produced in Example
11, the medium was removed and 100 ml of extraction buffer ((20 mM HEPES pH
7.5, 0.15 M NaCl, 1% Triton X-100, 0.1% SDS, 2 mM Na₃VO₄, 2 mM Na₄P₂O₇
and a cocktail of protease inhibitors (# 1836170) obtained from Boehringer Mannheim
(Indianapolis, IN) is added to each well and the plate is shaken on a rotating shaker for
25 5 minutes at 4°C. The plate is then placed in a vacuum transfer manifold and the extract
filtered through the 0.45 mm membrane bottoms of each well using house vacuum.
Extracts are collected in a 96-well catch/assay plate in the bottom of the vacuum
manifold and immediately placed on ice. To obtain extracts clarified by centrifugation,
the content of each well, after detergent solubilization for 5 minutes, is removed and
30 centrifuged for 15 minutes at 4°C at 16,000 x g.

Test the filtered extracts for levels of tyrosine kinase activity. Although many
methods of detecting tyrosine kinase activity are known, one method is described here.

Generally, the tyrosine kinase activity of a supernatant is evaluated by
determining its ability to phosphorylate a tyrosine residue on a specific substrate (a
35 biotinylated peptide). Biotinylated peptides that can be used for this purpose include
PSK1 (corresponding to amino acids 6-20 of the cell division kinase cdc2-p34) and

PSK2 (corresponding to amino acids 1-17 of gastrin). Both peptides are substrates for a range of tyrosine kinases and are available from Boehringer Mannheim.

The tyrosine kinase reaction is set up by adding the following components in order. First, add 10ul of 5uM Biotinylated Peptide, then 10ul ATP/Mg₂⁺ (5mM

- 5 . ATP/50mM MgCl₂), then 10ul of 5x Assay Buffer (40mM imidazole hydrochloride, pH7.3, 40 mM beta-glycerophosphate, 1mM EGTA, 100mM MgCl₂, 5 mM MnCl₂, 0.5 mg/ml BSA), then 5ul of Sodium Vanadate(1mM), and then 5ul of water. Mix the components gently and preincubate the reaction mix at 30°C for 2 min. Initial the reaction by adding 10ul of the control enzyme or the filtered supernatant.

- 10 The tyrosine kinase assay reaction is then terminated by adding 10 ul of 120mM EDTA and place the reactions on ice.

Tyrosine kinase activity is determined by transferring 50 ul aliquot of reaction mixture to a microtiter plate (MTP) module and incubating at 37°C for 20 min. This allows the streptavidin coated 96 well plate to associate with the biotinylated peptide.

- 15 Wash the MTP module with 300ul/well of PBS four times. Next add 75 ul of anti-phosphotyrosine antibody conjugated to horse radish peroxidase(anti-P-Tyr-POD(0.5u/ml)) to each well and incubate at 37°C for one hour. Wash the well as above.

- 20 Next add 100ul of peroxidase substrate solution (Boehringer Mannheim) and incubate at room temperature for at least 5 mins (up to 30 min). Measure the absorbance of the sample at 405 nm by using ELISA reader. The level of bound peroxidase activity is quantitated using an ELISA reader and reflects the level of tyrosine kinase activity.

25 **Example 20: High-Throughput Screening Assay Identifying Phosphorylation Activity**

- As a potential alternative and/or compliment to the assay of protein tyrosine kinase activity described in Example 19, an assay which detects activation (phosphorylation) of major intracellular signal transduction intermediates can also be used. For example, as described below one particular assay can detect tyrosine phosphorylation of the Erk-1 and Erk-2 kinases. However, phosphorylation of other molecules, such as Raf, JNK, p38 MAP, Map kinase kinase (MEK), MEK kinase, Src, Muscle specific kinase (MuSK), IRAK, Tec, and Janus, as well as any other phosphoserine, phosphotyrosine, or phosphothreonine molecule, can be detected by substituting these molecules for Erk-1 or Erk-2 in the following assay.
- 35

Specifically, assay plates are made by coating the wells of a 96-well ELISA plate with 0.1ml of protein G (1ug/ml) for 2 hr at room temp, (RT). The plates are then rinsed with PBS and blocked with 3% BSA/PBS for 1 hr at RT. The protein G plates are then treated with 2 commercial monoclonal antibodies (100ng/well) against Erk-1 and Erk-2 (1 hr at RT) (Santa Cruz Biotechnology). (To detect other molecules, this step can easily be modified by substituting a monoclonal antibody detecting any of the above described molecules.) After 3-5 rinses with PBS, the plates are stored at 4°C until use.

A431 cells are seeded at 20,000/well in a 96-well Loprodyn filterplate and cultured overnight in growth medium. The cells are then starved for 48 hr in basal medium (DMEM) and then treated with EGF (6ng/well) or 50 ul of the supernatants obtained in Example 11 for 5-20 minutes. The cells are then solubilized and extracts filtered directly into the assay plate.

After incubation with the extract for 1 hr at RT, the wells are again rinsed. As a positive control, a commercial preparation of MAP kinase (10ng/well) is used in place of A431 extract. Plates are then treated with a commercial polyclonal (rabbit) antibody (1ug/ml) which specifically recognizes the phosphorylated epitope of the Erk-1 and Erk-2 kinases (1 hr at RT). This antibody is biotinylated by standard procedures. The bound polyclonal antibody is then quantitated by successive incubations with Europium-streptavidin and Europium fluorescence enhancing reagent in the Wallac DELFIA instrument (time-resolved fluorescence). An increased fluorescent signal over background indicates a phosphorylation.

Example 21: Method of Determining Alterations in a Gene

Corresponding to a Polynucleotide

RNA isolated from entire families or individual patients presenting with a phenotype of interest (such as a disease) is isolated. cDNA is then generated from these RNA samples using protocols known in the art. (See, Sambrook.) The cDNA is then used as a template for PCR, employing primers surrounding regions of interest in SEQ ID NO:X. Suggested PCR conditions consist of 35 cycles at 95°C for 30 seconds; 60-120 seconds at 52-58°C; and 60-120 seconds at 70°C, using buffer solutions described in Sidransky, D., et al., Science 252:706 (1991).

PCR products are then sequenced using primers labeled at their 5' end with T4 polynucleotide kinase, employing SequiTherm Polymerase. (Epicentre Technologies). The intron-exon borders of selected exons is also determined and genomic PCR

products analyzed to confirm the results. PCR products harboring suspected mutations is then cloned and sequenced to validate the results of the direct sequencing.

PCR products is cloned into T-tailed vectors as described in Holton, T.A. and Graham, M.W., Nucleic Acids Research, 19:1156 (1991) and sequenced with T7
5 polymerase (United States Biochemical). Affected individuals are identified by mutations not present in unaffected individuals.

Genomic rearrangements are also observed as a method of determining alterations in a gene corresponding to a polynucleotide. Genomic clones isolated according to Example 2 are nick-translated with digoxigenindeoxy-uridine 5'-
10 triphosphate (Boehringer Mannheim), and FISH performed as described in Johnson, Cg. et al., Methods Cell Biol. 35:73-99 (1991). Hybridization with the labeled probe is carried out using a vast excess of human cot-1 DNA for specific hybridization to the corresponding genomic locus.

Chromosomes are counterstained with 4,6-diamino-2-phenylidole and
15 propidium iodide, producing a combination of C- and R-bands. Aligned images for precise mapping are obtained using a triple-band filter set (Chroma Technology, Brattleboro, VT) in combination with a cooled charge-coupled device camera (Photometrics, Tucson, AZ) and variable excitation wavelength filters. (Johnson, Cv. et al., Genet. Anal. Tech. Appl., 8:75 (1991).) Image collection, analysis and
20 chromosomal fractional length measurements are performed using the ISee Graphical Program System. (Inovision Corporation, Durham, NC.) Chromosome alterations of the genomic region hybridized by the probe are identified as insertions, deletions, and translocations. These alterations are used as a diagnostic marker for an associated disease.

25

Example 22: Method of Detecting Abnormal Levels of a Polypeptide in a Biological Sample

A polypeptide of the present invention can be detected in a biological sample, and if an increased or decreased level of the polypeptide is detected, this polypeptide is
30 a marker for a particular phenotype. Methods of detection are numerous, and thus, it is understood that one skilled in the art can modify the following assay to fit their particular needs.

For example, antibody-sandwich ELISAs are used to detect polypeptides in a sample, preferably a biological sample. Wells of a microtiter plate are coated with
35 specific antibodies, at a final concentration of 0.2 to 10 ug/ml. The antibodies are either monoclonal or polyclonal and are produced by the method described in Example 10.

The wells are blocked so that non-specific binding of the polypeptide to the well is reduced.

The coated wells are then incubated for > 2 hours at RT with a sample containing the polypeptide. Preferably, serial dilutions of the sample should be used to validate results. The plates are then washed three times with deionized or distilled water to remove unbounded polypeptide.

Next, 50 ul of specific antibody-alkaline phosphatase conjugate, at a concentration of 25-400 ng, is added and incubated for 2 hours at room temperature. The plates are again washed three times with deionized or distilled water to remove unbounded conjugate.

Add 75 ul of 4-methylumbelliferyl phosphate (MUP) or p-nitrophenyl phosphate (NPP) substrate solution to each well and incubate 1 hour at room temperature. Measure the reaction by a microtiter plate reader. Prepare a standard curve, using serial dilutions of a control sample, and plot polypeptide concentration on the X-axis (log scale) and fluorescence or absorbance of the Y-axis (linear scale). Interpolate the concentration of the polypeptide in the sample using the standard curve.

Example 23: Formulating a Polypeptide

The secreted polypeptide composition will be formulated and dosed in a fashion consistent with good medical practice, taking into account the clinical condition of the individual patient (especially the side effects of treatment with the secreted polypeptide alone), the site of delivery, the method of administration, the scheduling of administration, and other factors known to practitioners. The "effective amount" for purposes herein is thus determined by such considerations.

As a general proposition, the total pharmaceutically effective amount of secreted polypeptide administered parenterally per dose will be in the range of about 1 µg/kg/day to 10 mg/kg/day of patient body weight, although, as noted above, this will be subject to therapeutic discretion. More preferably, this dose is at least 0.01 mg/kg/day, and most preferably for humans between about 0.01 and 1 mg/kg/day for the hormone. If given continuously, the secreted polypeptide is typically administered at a dose rate of about 1 µg/kg/hour to about 50 µg/kg/hour, either by 1-4 injections per day or by continuous subcutaneous infusions, for example, using a mini-pump. An intravenous bag solution may also be employed. The length of treatment needed to observe changes and the interval following treatment for responses to occur appears to vary depending on the desired effect.

Pharmaceutical compositions containing the secreted protein of the invention are administered orally, rectally, parenterally, intracisternally, intravaginally,

intraperitoneally, topically (as by powders, ointments, gels, drops or transdermal patch), buccally, or as an oral or nasal spray. "Pharmaceutically acceptable carrier" refers to a non-toxic solid, semisolid or liquid filler, diluent, encapsulating material or formulation auxiliary of any type. The term "parenteral" as used herein refers to modes
5 of administration which include intravenous, intramuscular, intraperitoneal, intrasternal, subcutaneous and intraarticular injection and infusion.

The secreted polypeptide is also suitably administered by sustained-release systems. Suitable examples of sustained-release compositions include semi-permeable polymer matrices in the form of shaped articles, e.g., films, or microcapsules.
10 Sustained-release matrices include polylactides (U.S. Pat. No. 3,773,919, EP 58,481), copolymers of L-glutamic acid and gamma-ethyl-L-glutamate (Sidman, U. et al., Biopolymers 22:547-556 (1983)), poly (2- hydroxyethyl methacrylate) (R. Langer et al., J. Biomed. Mater. Res. 15:167-277 (1981), and R. Langer, Chem. Tech. 12:98-105 (1982)), ethylene vinyl acetate (R. Langer et al.) or poly-D- (-)-3-hydroxybutyric
15 acid (EP 133,988). Sustained-release compositions also include liposomally entrapped polypeptides. Liposomes containing the secreted polypeptide are prepared by methods known per se: DE 3,218,121; Epstein et al., Proc. Natl. Acad. Sci. USA 82:3688-3692 (1985); Hwang et al., Proc. Natl. Acad. Sci. USA 77:4030-4034 (1980); EP 52,322; EP 36,676; EP 88,046; EP 143,949; EP 142,641; Japanese Pat. Appl. 83-118008;
20 U.S. Pat. Nos. 4,485,045 and 4,544,545; and EP 102,324. Ordinarily, the liposomes are of the small (about 200-800 Angstroms) unilamellar type in which the lipid content is greater than about 30 mol. percent cholesterol, the selected proportion being adjusted for the optimal secreted polypeptide therapy.

For parenteral administration, in one embodiment, the secreted polypeptide is
25 formulated generally by mixing it at the desired degree of purity, in a unit dosage injectable form (solution, suspension, or emulsion), with a pharmaceutically acceptable carrier, i.e., one that is non-toxic to recipients at the dosages and concentrations employed and is compatible with other ingredients of the formulation. For example, the formulation preferably does not include oxidizing agents and other compounds that are
30 known to be deleterious to polypeptides.

Generally, the formulations are prepared by contacting the polypeptide uniformly and intimately with liquid carriers or finely divided solid carriers or both. Then, if necessary, the product is shaped into the desired formulation. Preferably the carrier is a parenteral carrier, more preferably a solution that is isotonic with the blood
35 of the recipient. Examples of such carrier vehicles include water, saline, Ringer's solution, and dextrose solution. Non-aqueous vehicles such as fixed oils and ethyl oleate are also useful herein, as well as liposomes.

The carrier suitably contains minor amounts of additives such as substances that enhance isotonicity and chemical stability. Such materials are non-toxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, succinate, acetic acid, and other organic acids or their salts; antioxidants such as ascorbic acid; low molecular weight (less than about ten residues) polypeptides, e.g., polyarginine or tripeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids, such as glycine, glutamic acid, aspartic acid, or arginine; monosaccharides, disaccharides, and other carbohydrates including cellulose or its derivatives, glucose, manose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; counterions such as sodium; and/or nonionic surfactants such as polysorbates, poloxamers, or PEG.

The secreted polypeptide is typically formulated in such vehicles at a concentration of about 0.1 mg/ml to 100 mg/ml, preferably 1-10 mg/ml, at a pH of about 3 to 8. It will be understood that the use of certain of the foregoing excipients, carriers, or stabilizers will result in the formation of polypeptide salts.

Any polypeptide to be used for therapeutic administration can be sterile. Sterility is readily accomplished by filtration through sterile filtration membranes (e.g., 0.2 micron membranes). Therapeutic polypeptide compositions generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

Polypeptides ordinarily will be stored in unit or multi-dose containers, for example, sealed ampoules or vials, as an aqueous solution or as a lyophilized formulation for reconstitution. As an example of a lyophilized formulation, 10-ml vials are filled with 5 ml of sterile-filtered 1% (w/v) aqueous polypeptide solution, and the resulting mixture is lyophilized. The infusion solution is prepared by reconstituting the lyophilized polypeptide using bacteriostatic Water-for-Injection.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration. In addition, the polypeptides of the present invention may be employed in conjunction with other therapeutic compounds.

Example 24: Method of Treating Decreased Levels of the Polypeptide

It will be appreciated that conditions caused by a decrease in the standard or normal expression level of a secreted protein in an individual can be treated by administering the polypeptide of the present invention, preferably in the secreted form. Thus, the invention also provides a method of treatment of an individual in need of an increased level of the polypeptide comprising administering to such an individual a pharmaceutical composition comprising an amount of the polypeptide to increase the activity level of the polypeptide in such an individual.

For example, a patient with decreased levels of a polypeptide receives a daily dose 0.1-100 ug/kg of the polypeptide for six consecutive days. Preferably, the polypeptide is in the secreted form. The exact details of the dosing scheme, based on administration and formulation, are provided in Example 23.

Example 25: Method of Treating Increased Levels of the Polypeptide

Antisense technology is used to inhibit production of a polypeptide of the present invention. This technology is one example of a method of decreasing levels of a polypeptide, preferably a secreted form, due to a variety of etiologies, such as cancer.

For example, a patient diagnosed with abnormally increased levels of a polypeptide is administered intravenously antisense polynucleotides at 0.5, 1.0, 1.5, 2.0 and 3.0 mg/kg day for 21 days. This treatment is repeated after a 7-day rest period if the treatment was well tolerated. The formulation of the antisense polynucleotide is provided in Example 23.

Example 26: Method of Treatment Using Gene Therapy

One method of gene therapy transplants fibroblasts, which are capable of expressing a polypeptide, onto a patient. Generally, fibroblasts are obtained from a subject by skin biopsy. The resulting tissue is placed in tissue-culture medium and separated into small pieces. Small chunks of the tissue are placed on a wet surface of a tissue culture flask, approximately ten pieces are placed in each flask. The flask is turned upside down, closed tight and left at room temperature over night. After 24 hours at room temperature, the flask is inverted and the chunks of tissue remain fixed to the bottom of the flask and fresh media (e.g., Ham's F12 media, with 10% FBS, penicillin and streptomycin) is added. The flasks are then incubated at 37°C for approximately one week.

At this time, fresh media is added and subsequently changed every several days. After an additional two weeks in culture, a monolayer of fibroblasts emerge. The monolayer is trypsinized and scaled into larger flasks.

pMV-7 (Kirschmeier, P.T. et al., DNA, 7:219-25 (1988)), flanked by the long terminal repeats of the Moloney murine sarcoma virus, is digested with EcoRI and HindIII and subsequently treated with calf intestinal phosphatase. The linear vector is fractionated on agarose gel and purified, using glass beads.

5 The cDNA encoding a polypeptide of the present invention can be amplified using PCR primers which correspond to the 5' and 3' end sequences respectively as set forth in Example 1. Preferably, the 5' primer contains an EcoRI site and the 3' primer includes a HindIII site. Equal quantities of the Moloney murine sarcoma virus linear backbone and the amplified EcoRI and HindIII fragment are added together, in the
10 presence of T4 DNA ligase. The resulting mixture is maintained under conditions appropriate for ligation of the two fragments. The ligation mixture is then used to transform bacteria HB101, which are then plated onto agar containing kanamycin for the purpose of confirming that the vector has the gene of interest properly inserted.

15 The amphotropic pA317 or GP+am12 packaging cells are grown in tissue culture to confluent density in Dulbecco's Modified Eagles Medium (DMEM) with 10% calf serum (CS), penicillin and streptomycin. The MSV vector containing the gene is then added to the media and the packaging cells transduced with the vector. The packaging cells now produce infectious viral particles containing the gene (the packaging cells are now referred to as producer cells).

20 Fresh media is added to the transduced producer cells, and subsequently, the media is harvested from a 10 cm plate of confluent producer cells. The spent media, containing the infectious viral particles, is filtered through a millipore filter to remove detached producer cells and this media is then used to infect fibroblast cells. Media is removed from a sub-confluent plate of fibroblasts and quickly replaced with the media
25 from the producer cells. This media is removed and replaced with fresh media. If the titer of virus is high, then virtually all fibroblasts will be infected and no selection is required. If the titer is very low, then it is necessary to use a retroviral vector that has a selectable marker, such as neo or his. Once the fibroblasts have been efficiently infected, the fibroblasts are analyzed to determine whether protein is produced.

30 The engineered fibroblasts are then transplanted onto the host, either alone or after having been grown to confluence on cytodex 3 microcarrier beads.

35 It will be clear that the invention may be practiced otherwise than as particularly described in the foregoing description and examples. Numerous modifications and variations of the present invention are possible in light of the above teachings and, therefore, are within the scope of the appended claims.

 The entire disclosure of each document cited (including patents, patent applications, journal articles, abstracts, laboratory manuals, books, or other

disclosures) in the Background of the Invention, Detailed Description, and Examples is hereby incorporated herein by reference. Further, the hard copy of the sequence listing submitted herewith and the corresponding computer readable form are both incorporated herein by reference in their entireties.

5

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Applicant's or agent's file reference number	PZ017PCT	International application No.
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>125</u> , line <u>7</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution American Type Culture Collection ("ATCC")	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit 28 AUGUST 1997	Accession Number 209225
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

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B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution American Type Culture Collection ("ATCC")	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit 28 AUGUST 1997	Accession Number 209226
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B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution American Type Culture Collection ("ATCC")	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit 04 SEPTEMBER 1997	Accession Number 209235
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>128</u> . line <u>3-5</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution American Type Culture Collection ("ATCC")	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit 04 SEPTEMBER 1997	Accession Number 209236
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

For receiving Office use only <input checked="" type="checkbox"/> This sheet was received with the international application Authorized officer Sonya D Barnes	For International Bureau use only <input type="checkbox"/> This sheet was received by the International Bureau on: Authorized officer
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Applicant's or agent's file reference number	PZ017PCT	International application no.
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 129, line 17	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution American Type Culture Collection ("ATCC")	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit 12 SEPTEMBER 1997	Accession Number 209241
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable) The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

For receiving Office use only	For International Bureau use only
<input checked="" type="checkbox"/> This sheet was received with the international application	<input type="checkbox"/> This sheet was received by the International Bureau on:
Authorized officer <i>Sonye Barnes</i>	Authorized officer

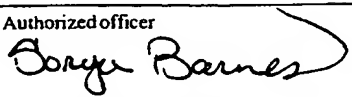
217

Applicant's or agent's file reference number	PZ017PCT	International application
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>142</u> . line <u>19</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution American Type Culture Collection ("ATCC")	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit 12 SEPTEMBER 1997	Accession Number 209242
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

For receiving Office use only	For International Bureau use only
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Form PCT/RO/134 (July 1992)

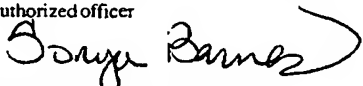
218

Applicant's or agent's file reference number	PZ017PCT	International application No.
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 134, line 9	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution American Type Culture Collection ("ATCC")	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit 12 SEPTEMBER 1997	Accession Number 209243
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

For receiving Office use only <input checked="" type="checkbox"/> This sheet was received with the international application Authorized officer 	For International Bureau use only <input type="checkbox"/> This sheet was received by the International Bureau on: Authorized officer
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Form PCT/RO/134 (July 1992)

What Is Claimed Is:

1. An isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence at least 95% identical to a sequence selected from the group consisting of:

(a) a polynucleotide fragment of SEQ ID NO:X or a polynucleotide fragment of the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

(b) a polynucleotide encoding a polypeptide fragment of SEQ ID NO:Y or a polypeptide fragment encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

(c) a polynucleotide encoding a polypeptide domain of SEQ ID NO:Y or a polypeptide domain encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

(d) a polynucleotide encoding a polypeptide epitope of SEQ ID NO:Y or a polypeptide epitope encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

(e) a polynucleotide encoding a polypeptide of SEQ ID NO:Y or the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X, having biological activity;

(f) a polynucleotide which is a variant of SEQ ID NO:X;

(g) a polynucleotide which is an allelic variant of SEQ ID NO:X;

(h) a polynucleotide which encodes a species homologue of the SEQ ID NO:Y;

(i) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(h), wherein said polynucleotide does not hybridize under stringent conditions to a nucleic acid molecule having a nucleotide sequence of only A residues or of only T residues.

2. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding a secreted protein.

3. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding the sequence identified as SEQ ID NO:Y or the polypeptide encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X.

4. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises the entire nucleotide sequence of SEQ ID NO:X or the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X.

5. The isolated nucleic acid molecule of claim 2, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.

6. The isolated nucleic acid molecule of claim 3, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.

7. A recombinant vector comprising the isolated nucleic acid molecule of claim 1.

8. A method of making a recombinant host cell comprising the isolated nucleic acid molecule of claim 1.

9. A recombinant host cell produced by the method of claim 8.

10. The recombinant host cell of claim 9 comprising vector sequences.

11. An isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence selected from the group consisting of:

- (a) a polypeptide fragment of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;
- (b) a polypeptide fragment of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z, having biological activity;
- (c) a polypeptide domain of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;
- (d) a polypeptide epitope of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;
- (e) a secreted form of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;
- (f) a full length protein of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

- (g) a variant of SEQ ID NO:Y;
- (h) an allelic variant of SEQ ID NO:Y; or
- (i) a species homologue of the SEQ ID NO:Y.

12. The isolated polypeptide of claim 11, wherein the secreted form or the full length protein comprises sequential amino acid deletions from either the C-terminus or the N-terminus.

13. An isolated antibody that binds specifically to the isolated polypeptide of claim 11.

14. A recombinant host cell that expresses the isolated polypeptide of claim 11.

15. A method of making an isolated polypeptide comprising:

- (a) culturing the recombinant host cell of claim 14 under conditions such that said polypeptide is expressed; and
- (b) recovering said polypeptide.

16. The polypeptide produced by claim 15.

17. A method for preventing, treating, or ameliorating a medical condition, comprising administering to a mammalian subject a therapeutically effective amount of the polypeptide of claim 11 or the polynucleotide of claim 1.

18. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:

- (a) determining the presence or absence of a mutation in the polynucleotide of claim 1; and
- (b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or absence of said mutation.

19. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:

- (a) determining the presence or amount of expression of the polypeptide of claim 11 in a biological sample; and
- (b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the polypeptide.

20. A method for identifying a binding partner to the polypeptide of claim 11 comprising:

- (a) contacting the polypeptide of claim 11 with a binding partner; and
- (b) determining whether the binding partner effects an activity of the polypeptide.

21. The gene corresponding to the cDNA sequence of SEQ ID NO:Y.

22. A method of identifying an activity in a biological assay, wherein the method comprises:

- (a) expressing SEQ ID NO:X in a cell;
- (b) isolating the supernatant;
- (c) detecting an activity in a biological assay; and
- (d) identifying the protein in the supernatant having the activity.

23. The product produced by the method of claim 20.

<110> Rosen et al.
Human Genome Sciences, Inc.

<120> 101 Human Secreted Proteins

<130> PZ017.PCT

<140> Unassigned

<141> 1998-10-01

<150> 60/060,837

<151> 1997-10-02

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<151> 1997-10-02

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aaaaactctt	cagctttttc	cagtgtgtct	ccttaacagt	aactttacca	cttgaaatct	1140
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<210> 16

<211> 1036

<212> DNA

<213> Homo sapiens

<400> 16

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tgataacaac	agcagcacc	tggagatact	cttaaaagat	gatgatgatg	attcagactc	180
tgatggtgat	ggcaaagatc	ttgtgcctca	agcagccatt	gagtatggca	ggatcctgac	240
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gtaccacttt	ctccggaccc	agaagatcat	ctggatgcct	caggaactgg	atgcatttca	360
gccatacccc	attgaaattg	tgccagggaa	ggctctcggt	ggcaatttca	gtcaagcctg	420
tgaccccaag	attcagaagg	acttgaaaat	caaagcccat	gtcaatgtct	ccatggatac	480
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gagtgtgtat	acccaggctt	gtctggaagg	agaaggcctt	tgctgcctga	aagtcwmaaa	960
aaaaaaaaaa	aaaackcgag	ggggggcccg	gtaccagct	tttgttcct	ttagtgaggg	1020
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<210> 17

<211> 1014

<212> DNA

<213> Homo sapiens

<400> 17

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ctatgccatc	atgtcaagac	caagatgata	tggttgagaa	atctggatca	gagactcctg	360
atggtccatt	gtcccctggg	aaaatggagg	atatctctcc	tgtgcagaca	gagccctgg	420
attcagttag	ggagagatta	catggaggca	aaggtctgcc	tttttatgca	gggctttctc	480
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atttttcaga	gccctttatg	gtcctgatag	cctttatctt	gacatttcct	gggaactggg	660
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ggtttcaaaa	caaaaccatg	gttagaacgg	taggtgtaag	gggaagatga	aattgactta	960
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<210> 18

<211> 1287

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (1282)

<223> n equals a,t,g, or c

<400> 18

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gatctgacaa	atgtatgttt	aaacatgaat	tagaagagtt	gagaactacc	attatgtata	180
gggattctca	tagtgtcttg	gcccttaatt	ggaaagtgtg	ggcaacttta	aagtactttt	240
tactgtatgt	tataattctt	tataacttag	agagagacaa	tggtcactca	aactatgaga	300
actatgaatt	aggagataaa	agttttaaatt	tgttgttgtt	ttataacagt	atgtacaagt	360
tagttttccc	ttatatattt	acgttttcaa	gttttttaatt	ctcatcatat	acatccatac	420
tctataaaa	gttttatatt	caaagaactg	taaaatccta	aacattagtt	ttcactattg	480
aaattgtttt	ttaaagatag	gcataaatag	ttgtccttag	acttattcat	acaaatatag	540
tcatttactt	ctatgtagtt	tgagattctg	agagttattc	caactttatg	aagattgatt	600
tcaatgtgac	tgctaagtc	taaaagattc	agaaagaaaa	tttatatatt	attgatttaa	660
atatcatcct	ttaaatatgt	tgtataacat	tcaatatagt	ttatgtatca	gtgattgtat	720
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taataaatat	aacctgtaaa	ccacaaaaaa	aaaaaaaaa	aaactcgagg	gggggcccgg	1260
tacccaatcg	csgwgtgatg	gngctat				1287

<210> 19

<211> 1105

<212> DNA

<213> Homo sapiens

<400> 19

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tgattattat	tattcccttc	ttaacacaca	aagaaggagg	ggatccaaaa	ataacagtgt	180
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tctggacaac	cctggcaact	cggaacatga	aggagagaac	aagaattccc	tgtgcttttc	360
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attttactgc	ctaactctata	aaggaggatt	aacagcagca	cgctgctttg	gcatagagca	480
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aagtgtgtgg	tggccatcct	ttcccttttg	agagtgggt	agaggtagtt	aaccttctctg	900
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taaaactgct	tcctttgcca	aacacaaaga	atgggtctgga	gttggatatt	agcaaacagc	1020
aaaccacata	aagaagacaa	aaaaaaaaaa	aaaaaaaaaa	ctcgaggggg	ggcccgtacc	1080
caatcgccctg	tgatgtatcg	tatac				1105

<210> 20

<211> 1089

<212> DNA

<213> Homo sapiens

<400> 20

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gccccaaagc	ccagcttcta	taacttgttc	atggctaccg	tacatagaag	caccaggac	180
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ctataaggca	ggaaaaaaga	agaagattaa	grttatccat	gatttcatca	ctcgggatga	300
ccagtgttat	tgtactat	atcttaaaag	tgtttttcaa	atatttttct	acaacatcat	360
ttttaaatgc	ttgcatacat	tttatacata	aatgtaaact	agttaactaa	ttcctctatt	420
gctggaattt	taagatgtct	ctaaatgata	taaacaatat	ttcaaatttt	gtgattggga	480
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cgagaccagc	ctggccaaca	tggtgaaacc	ccgtctctac	caaaaataca	aaaattagct	900
gggtgtggag	gtgcatgcct	ataatcccag	ctactcagga	ggctgaggca	ggagaatcgc	960
ttgaaccggg	gaggcggtgg	ttgcagttag	cgaagatagt	gccattgcac	tccagcctgg	1020
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aaactcgta						1089

<210> 21

<211> 2831

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (182)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (219)

<223> n equals a,t,g, or c

<400> 21

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gnaagataga	gaagactctc	cagaaagatg	cagcgacana	atkgaggaaa	agaaagcgag	240
aagaggcaga	tctcccaaag	gtgaattcaa	agatgaagag	gagactgtga	cgacaaagca	300
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tacctcccca	tgttatgttg	aaaatttttt	tattaaattg	ataaaacttt	atttccatta	2760
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<210> 22

<211> 1448

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (1422)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (1434)

<223> n equals a,t,g, or c

<400> 22

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aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaanaaaaaa	1440
aaaaaggg						1448

<210> 23
 <211> 1211
 <212> DNA
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (131)
 <223> n equals a,t,g, or c

<220>
 <221> SITE
 <222> (915)
 <223> n equals a,t,g, or c

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 cgatggctgt ggaaaccttt ggcttcttca tggcaactkt ggggctgctg atgctggggg 240
 tgactctgcc aaacagctac tggcgagtgt ccactgtgca cgggaacgtc atcaccacca 300
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<210> 24
 <211> 1060
 <212> DNA
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (453)
 <223> n equals a,t,g, or c

<220>
 <221> SITE
 <222> (1045)
 <223> n equals a,t,g, or c

<400> 24
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 cttaacatgc tgtttattta cttgtttgta ttccccatta gaataggctc tgagaaagca 120
 aagactgtat ctgtcttgct tatcattgta tccctgacag ctcgcccact ggctggcttt 180

taataagcac	accataaata	tttacttgaa	atactcattt	ttaaaatgaa	cagatgaatg	240
aatgatagat	ggatgggtgga	tggcattatg	tagctaaaaa	ttgtgtcctg	tctctaccta	300
tttttgaaga	ccatccttta	gtttgcgttt	cctgccatgt	ttgagggggc	tttttttgg	360
ccataactct	tgtcttttat	tcaaattaaa	acaccgaaca	aaagcacatt	cgattattgr	420
ccatgrgggt	ttttattcyg	ctgtcagtg	cancycmtg	tctaaatccc	cygggggtcaa	480
acttacatat	atctggatag	cccttttkga	tgacgatgg	agtctaattt	gtgtgttatg	540
tgtcttgaa	atgttttgct	gtaaagacac	tagaactgaa	ttttgcttta	ttgccaatga	600
tgtatgaatg	taaaaaaaac	aactcagtaa	cattcaaacc	aatttccaag	tttgttcttc	660
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catacaccat	aaaattcacc	attttaaaagt	ttccaattta	gtgggttttta	gtatgtttac	780
agagtcatgc	aaccatcacc	acagtatcat	tgcaggatgt	ttttatcatc	cctcaaagaa	840
atccagaccc	acaggaggct	gaggcaggag	aatcgcttga	acccggaagg	cggagggttc	900
agttagtccg	agatagcgcc	actgcactcc	agcctagtga	cagagcaaga	ctctgtctca	960
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	tcgaaggggg	1020
ggcccggtac	ccaatcgtcc	ctatnatgag	tcgtattaca			1060

<210> 25

<211> 1057

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (348)

<223> n equals a,t,g, or c

<400> 25

gaattcggca	cgagcggcac	gagatttttag	gtaaatgacg	aagggaatgt	ggtgaatgtc	60
actgtccaga	gccataaatc	agacaaaacc	atacatagca	tgtgaaaaa	cttttgaat	120
ggaacaccca	acaaatgaca	cctaacctgt	ctgtgatcca	acaagtccga	taacatgctg	180
ctgtatttgt	attctctggg	aatctcagta	ttataattt	catttcccac	aaattctagc	240
attcatgtaa	ggaaaaacat	ggctaataca	tatcttaaag	gggcaatctt	tcagagcagt	300
ggtttttcaa	gtgtggccgg	acagcattgg	cagcatctta	atctcctngg	gactttgtta	360
aaaatgcaaa	ttctcagccc	caccctagtc	ctactgaatt	gggaaactgg	cgtgggaccc	420
agcagtcttt	gttttaacat	gttctccaag	tgattctgat	gcctgttcaa	acttgggaaa	480
cactttttaga	gcacttgagg	aacctaaaag	atgactgggt	cagcattttg	tgtggtagat	540
aagaaagaaa	ttatcacaaa	aaatcagaaa	tgaacagtga	gagaaaaata	ggaccccaga	600
cagttttatc	cttccatttg	ctgttttaaa	agtgtgagcc	tgccaagtca	acaagtatgc	660
cttttagcgca	catgtaaaata	gcctgcactt	cctaaatctc	gtgtggcctc	ccatggttac	720
attcttcaaa	ggtwaactga	gttgagagga	agattcagca	tttaaaagag	aagggttgaa	780
aaagattgtg	tgtgtgtgtg	tgtgtgtgtt	taattggccc	agggttactt	aaataaatca	840
taaccatttt	gccacattct	gtaactgttt	agctaaggtc	aaattaagtt	taccctatgg	900
attttgtttc	atcttttgtt	tcgtgtatat	actgtttgcc	tttttcataa	aaatcttggg	960
tttgttatat	attgttcctg	ttatttttga	catctttgct	attgtaaata	aattactatt	1020
ttgttttaag	ttaaaaaaa	aaaaaaaaaa	acwcgta			1057

<210> 26

<211> 980

<212> DNA

<213> Homo sapiens

<400> 26

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tccagatgct	ggcggatccc	cgctccttcg	actccaacgc	cttcacgctt	ctcctccggg	120
cggcattcca	gagtctgctg	gacgcccagg	cggacgaggc	cgtgttagat	catccagact	180
tgaacatat	cgaccagtg	gttttaaaac	attgtcatgc	agcagctgca	acttacatac	240

tagaggcagg	aaagcaccga	gctgacaagt	caactctaag	cacttatcta	gaagactgta	300
aatttgacag	agagcgaata	gaactgtttt	gcacggaata	tcagaataat	aagaattccc	360
tagaaatcct	actgggaagt	ataggcagat	ctctccctca	tataacggat	gtttcttggc	420
gcttggaata	tcagataaag	accaatcaac	ttcataggat	gtacagacct	gcatatttgg	480
tgaccttaag	tgtacagaac	actgattccc	catcctatcc	agagattagt	tttagttgca	540
gcatggaaca	attacaggac	ttggtgggga	aacttaaaga	tgcttcgaaa	agcctggaaa	600
gagcaactca	gttgtaactt	ggggaagtta	acgatccgcc	cgagtgcaga	ggaaaaccag	660
aaacgccttg	ccttcagctg	aaccaccgtt	tgtgcgagct	ggatgtcctt	ttcagtagaa	720
aagaattttc	cttttgaatt	tataccattc	atcaattttg	acactttaaa	aacgtgtgaa	780
agggttaaga	gggaaagata	ctgcccaagt	atttgaatcg	tttagtagta	actgtccatt	840
tatcctatct	tgatcttttt	caagtcttct	gaaaggaagt	agacagtatt	acaccctgaa	900
taaataaggt	gttgtttttc	acaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	960
aaaaaaaaaa	aagggcggcc					980

<210> 27

<211> 755

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (748)

<223> n equals a,t,g, or c

<400> 27

gaattcggca	cgagattgtg	cacatgtacc	ctaaaactta	agatgtaata	ataataaaat	60
aaaaataaaat	aaattaaaaa	ataaaaataa	aaacarattt	aatgataggg	tacttaatga	120
aagtwttggt	ggtccttgaa	tgacgtatct	tacactacat	atgtacctac	ttttctattc	180
tcctcctcag	atgggaaagg	tctagataaa	ctggcctcta	tcccgcagct	cttctccaca	240
atggttaaga	acagttcaac	acggaggacc	agcagtaaat	gacctttaaa	aagtgtaata	300
ataactattg	cccaaaataa	tcttattaat	catagaaaat	ggcttctatt	cttctgctcc	360
ttgttctgtc	acacagctgt	tgctgtaaaa	acacttgttt	acaggttcta	tgtaattttg	420
actcagttcca	taatctctcc	accctaattt	taaaaattat	catcagggtg	gatgtgctag	480
tatactaaga	aacatctgtt	aatattatct	attttcttta	tttaattctt	ttcatagatt	540
cacttgtttt	aaaatatctt	aggtttataa	tctctttgca	aagctcaata	aatcatttta	600
acagctaaaa	ataaaaactt	aaaaatgaac	tccagataaa	tatgaagatt	caaaaactatg	660
tggaatctct	gccccctct	taatactcac	caataaattc	tacttctgt	cmaaaaaaaa	720
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaa			755

<210> 28

<211> 946

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (5)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (23)

<223> n equals a,t,g, or c

<400> 28

tcgcnactat	agggaaactgg	tcnctgcagg	tccggtcgga	attccgggtc	gacccacgcg	60
------------	-------------	------------	------------	------------	------------	----

tccggtaaat	gttttatgtg	ttcgctact	gatcccatc	gttgcttcta	ttgtaaatat	120
ttgtcatttg	tatttattat	ctctgtgtt	tccccctaag	gcataaaatg	gtttactgtg	180
ttcatttgaa	cccatttact	gatctctgtt	gtatatTTTT	catgccactg	ctttgttttc	240
tcctcagaag	tcgggtagat	agcattttcta	tcccatccct	cacgttattg	gaagcatgca	300
acagtattta	ttgctcagg	tcttctgctt	aaaactgagg	aaggtccaca	ttcctgcaag	360
cattgattga	gacatttgca	caatctaaaa	tgtaaacaaa	gtagtcatta	aaaatacacc	420
ctctacttgg	gctttatact	gcatacaaat	ttactcatga	gccttccttt	gaggaaggat	480
gtggatcttc	aaataaagat	ttagtgttta	ttttgagctc	tgcattctaa	caagatgac	540
tgaacacatc	tcctttgtat	caataaatag	ccctgttatt	ctgaagtgag	aggaccaagt	600
atagtaaaat	gctgacatct	aaaactaaat	aaatagaaaa	caccaggcca	gaactatagt	660
catactcaca	caaagggaga	aatttaaact	cgaaccaagc	aaaaggcttc	acggaaatag	720
catggaaaaa	caatgcttcc	agtggscact	tcctaaggag	gaacaacccc	gtctgatctc	780
agaattggca	ccacgtgagc	ttgctaagtg	ataatatctg	tttctactac	ggatttaggc	840
aacaggacct	gtacattgtc	acattgcatt	atttttcttc	aagcgtaaat	aaaagtttta	900
aataaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaag	gcggcc		946

<210> 29

<211> 971

<212> DNA

<213> Homo sapiens

<400> 29

gcttctatcc	atttattcaa	gcacatatg	gtcacctact	gtgtgcctgg	cactcatgtc	60
acaaagataa	gttcctgatt	cggtagactt	actgagcacc	tgtgtgtgtc	agggagctga	120
gctatgggat	gggaatggga	gtaaacaagg	tacttttyac	ttttttcttt	ttttctcac	180
tgctagacgg	tgtgggaact	tctcactcat	tggcttcttt	cccacacacc	tgaagagcac	240
tgactgtgtg	ccgggcacta	gtgatacaaa	agagtgtgac	agttgttcag	tctgcatttt	300
cgatcatggg	ctacatgccg	agtgtctggg	cacagagatg	aacaagatcg	gttccttcac	360
ttcttcatgc	cacaagtgtt	tattgagcac	ctgtgtgcca	ggcctcacag	actcccagtt	420
gggttgaaga	atggttgact	gagtttgatt	cttctgtac	cctcggtcgt	ctgagctgtg	480
tgcagacaac	atccccccac	cacccaagag	ggagggtagc	tcttccgcca	ccaggggcaa	540
gcacaggctc	tgggtggccc	acgccacatg	ttagccccc	tggagggggc	gccagttgga	600
gacgggggct	gggtgtccct	ggccactcc	cggteccctg	tgtttacct	ccttgccctt	660
gtgtctcagg	tgtgttcctt	gcctgcttga	tgaagtgtct	ctgttcaagc	ccttggtggg	720
atcatgtgtt	tgggggcttt	taggggaccc	agctgcactg	gggcactgcc	cgtggcctgg	780
gtaggacatt	tcccagcaag	ggctggagga	gttgccgtgc	cttcagcctg	aatcgaatgt	840
cagaaccagc	cagcgggtgt	tcaccctctt	ggggataact	tgcttagttt	tttaataaat	900
gttcctgggt	ggttttcaca	gcaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	960
aaaaaaaaaa	g					971

<210> 30

<211> 1008

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (421)

<223> n equals a,t,g, or c

<400> 30

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gctgtgcttt	gagggactaa	aggaagcctg	tatcttgttg	tgaggggtcc	acctcacaag	120
ttacagatct	cagttccatt	tggctctagc	agcaatgtgg	ccacttctgt	tgcggttact	180
ctttcttcac	ctttttcttg	ccaaaaataa	acttatcttt	aaatgaaaac	taaattatct	240
cttatatttt	ggtcctttgt	tatagctgag	attgggaatt	tttctttctt	tcttgaatcc	300

ttacttccct	accctgcctc	cccaccaatg	gaaatctgtg	cttcataagc	attttagatt	360
ccagaaagct	cttttaggta	aactacaacc	ctctcacctc	aaagaatttg	tgggccaggg	420
naagtcagtg	acttatgtga	agtcttgctg	ctaattaatg	gtagagctgg	agttaggaca	480
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aatttttctg	gatactactc	ccataaaatg	ttctttgaaa	aatacttgct	tctttctagt	600
ttttctcgcc	tggtttaa	attgtcctga	gtgtgggaac	cccataactg	tcttgtgggt	660
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gcttattgga	cacatggatt	ttcttcagat	ttgcacttac	tgctagctct	gctttttatg	840
caggagaaaa	gcccagagtt	caactgtgtg	cagaacaact	ttctaacaaa	catttattaa	900
tccagcctct	gcctttcatt	aaatgtaacc	ttttgccttc	caaattaaag	aactccatgc	960
cactcctcaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaa		1008

<210> 31

<211> 990

<212> DNA

<213> Homo sapiens

<400> 31

aattcggcac	gagtggacaa	ccatcaggga	gccaggacac	agaggggcag	agcaagtcag	60
cattggcgcc	ccttctcag	atccctatca	tcttgggaaa	cagtagccca	gaggttcagg	120
aagatgtaa	cttaaatgtt	cgggggtgcc	cagtctgttc	agcatggctg	aaatccacac	180
tccgtattct	tccttgaaga	aactgttatc	tttactcaat	ggcttcgtgg	ctgtgtctgg	240
catcatccta	gttggcctgg	gcattgggtg	taaatgtgga	ggggcctctc	tgacgaatgt	300
cctcgggctg	tcctccgcat	acctccttca	cgttggcaac	ctgtgcctgg	tgatgggatg	360
catcasggtg	ctgcttggct	gtgccgggtg	gtatggagcg	actaaagaga	gcagaggcac	420
gytcttggtt	gttggagatg	tggccttgga	acacamcttc	gtgaccctga	ggaagaatta	480
cagaggttac	aacgagccag	acgactattc	tacacagtgg	aacttgggtc	tggagaagct	540
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gggccacacy	taccacagga	gttgctgtaa	atccatcgga	agtgtgtcct	gtgacggacg	660
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gatgagacac	ctgggcccac	ctggctgctg	gagattcagt	ctcagtttta	tttctctgtg	900
gcactcactg	cttctggagg	ggagactgtt	aataaaagat	ttgggaaaaa	aaaaaaaaaa	960
aaaaaaaaaa	aaaaaaaaaa	aaaaactcga				990

<210> 32

<211> 1131

<212> DNA

<213> Homo sapiens

<400> 32

gaattcggca	cgaggcctat	gtcatcctgg	ctgtgtgctt	ggggggaatg	atcgggatct	60
ctgccagctt	ctcagccctc	ctggagcaga	tcctctgtgc	aagcggccac	tccagtgggt	120
tttcggcctt	ctgtggcgct	ctcttcacga	cgtttgggat	cctgggggca	ctggctctcg	180
gcccctatgt	ggaccggacc	aagcacttca	ctgaggccac	caagattggc	ctgtgcctgt	240
tctctctggc	ctgcgtgcc	tttgccttgg	tgtcccagct	gcagggacag	acccttgccc	300
tggctgccac	ctgctcgctg	ctcgggctgt	ttggcttctc	ggtgggcccc	gtggccatgg	360
agttggcggt	cgagtgttcc	ttccccgtgg	gggagggggc	tgccacaggc	atgatctttg	420
tgctggggca	ggccgaggga	atactcatca	tgctggcaat	gacggcactg	actgtgcgac	480
gytcggagcc	gtccttgtcc	acctgccagc	agggggagga	tcacttgac	tggacagtgt	540
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gcgcttgta	gtccagggtg	cccgccacat	cgatggaggc	gaactggaac	atctgggtcca	1020
cctgcggg	ggggcgaaag	ggctccttgc	gggtccggg	agcgaattac	aagcgcgcac	1080
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<210> 33

<211> 1293

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (1)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (7)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (8)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (25)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (396)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (1271)

<223> n equals a,t,g, or c

<400> 33

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gctcctatat	ccctccctgt	aagagagaaa	atcagaagaa	tttgaaagt	gtcatgaatt	180
ggcaacagta	ctggaaagat	gagattggtt	cccagccatt	tacttgctat	tttaatcaac	240
atcaaagacc	agatgatgtg	cttctgcac	gcactcatga	tgagattgtc	ctcctgcatt	300
gcttccctctg	ggccctgggtg	acatttgttg	tggcggttct	cattgtggtc	ctgaccatct	360
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gtagtataca	aaccattatg	atttatgcta	cttaaaaata	gtggctctgtg		780
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gacgtctgct	tggaatga	atagtatact	ggtaactcag	tctccagtca	cctctgtgct	1020
tcttaagcaa	gagattctaa	aagattggga	aaacatatcc	tccaamacct	gcctttgcct	1080
aaccattatt	tttcaccaga	ttacttctta	agagagggag	gtgattctga	agaaggcttc	1140
tatctcaaaa	agcactgggc	ttccttattc	atctgttctt	gttgtttttg	acggagttaa	1200
aaaagtttgt	gtgcaatata	atataaatga	tgtgaaggac	actcttaaaa	aaaaaaaaaa	1260
aaaaaaaaat	ngctgcggcc	gacaaggga	ttc			1293

<210> 34

<211> 1014

<212> DNA

<213> Homo sapiens

<400> 34

ggcacgaggt	cagccagaac	atgtctttca	acctgcaatc	atcaaagaaa	ctgttcattt	60
tcttaggaaa	atcactgttt	agtcttctgg	aggctatgat	ttttgcctta	ctcccaaagc	120
cacggaagaa	cggtgctggt	gaaatagtcc	tcatcacagg	tgctggaagt	ggactcggaa	180
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aagaagtcgg	cgatgtttcc	atcctaatac	acaatgccgg	aatcgtaaca	ggcaaaaagt	420
tccttgactg	tccagatgag	cttatggaaa	agtcatttga	tgtgaatttc	aaagcacatt	480
tatggactta	taaagccttt	ctacctgcta	tgattgctaa	tgaccatgga	catttggttt	540
gcatttcaag	ttcagctgga	ttaagtggag	taaatgggct	ggcagattac	tgtgcaagta	600
aatttgcagc	ctttgggttt	gctgaatctg	tatttgtaga	aacatttgct	caaaaacaaa	660
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gtactacagg	ctgtccttct	ctgttgccaa	ttctggaacc	aaaaatagca	gttgaaaaaa	780
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acagttttac	tcccaaatcc	caccagga	aaagccactt	twaaaaatac	ctgataaatt	960
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<210> 35

<211> 1222

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (4)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (52)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (78)

<223> n equals a,t,g, or c

<400> 35

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ggctgacca	cgcgctcnga	aatttacaat	ttctgacat	ccacaacct	ttgatccact	120

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gttaaagaac tgcataaggat atttcctaaa aactttggaa gacccagatt tgaatgtgag 180
aagagtagcc ttgggtcacat ttaattcagc agcacataac aagccatcat taataagggg 240
tctattggat actgttcttc cacatcttta caatgaaaca aaagttagaa aggagcttat 300
aagagaggta gaaatgggtc catttaaaca tacgggtgat gatgggtctgg atattagaaa 360
ggcagcattt gagtgtatgt acacacttct agacagttgt cttgatagac ttgatatctt 420
tgaatttcta aatcatgttg aagatggttt gaaggacat tatgatatta agatgctgac 480
atttttaatg ttgggtgagac tgtctaccct ttgtccaagt gcagtactgc agaggttgga 540
ccgacttggt gagccattac gtgcaacatg tacaactaag gtaaaggcaa actcagtaaa 600
gcaggagttt gaaaaacaag atgaattaaa gcgatctgcc atgagagcag tagcagcact 660
actaaccatt ccagaagcag agaagagtcc actgatgagt gaattccagt cacagatcag 720
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<210> 36

<211> 901

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (895)

<223> n equals a,t,g, or c

<400> 36

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acataggtea cctcattcat gaaggcctac agaagaacac ttctctgtgg gtactgtata 180
acatggcttc attttactgg agaattaaga atgagccata tcaggtagta gaatgtgcca 240
tgcgagcact tcacttctct tccaggcaca ataaagacat tgccctgggc aacctggcaa 300
acgttctaca cagagcacac ttctctgtct atgctgtctg cgtgggtccat gcagctctgg 360
atgacagtga cttcttcacc agctattaca ctttggggaa tatatatgca atgcttgggg 420
aatataacca ctcatgtctc tgttatgacc acgctttgca ggccagacct gggtttgagc 480
aagctataaa gaggaagcat gctgtcctat gtcagcaaaa actggagcag aaattggagg 540
ctcagcatag atctctccag cgaacactga atgagttaaa agagtatcaa aagcagcatg 600
accactacct gagaccagga aatcctagaa aaacataaac tgattcagga ggagcaaactc 660
ttaagaaata tcattcatga gactcagatg gcaaaaagarg cacaattagg aaatcatcag 720
atatgccgac tgggtcaacca gcagcatagt ttacattgcc agtgggamca gcctgtwcgc 780
tatcatcggt gagatatctt tgaaaatgtg gactatgttc argtcttttt cttggtccar 840
tctaattctt ataaacgttt gctttataaa gattttttta aactttaaaa aaacngcacg 900
a 901

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<210> 37

<211> 954

<212> DNA

<213> Homo sapiens

<400> 37

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gaattcggca cgagccca ccaaactgt ggacgccgac ccgggaccgc cgtgggtgg 60
ctgctggctc actcgaccgt catggagacc ctggggggccc ttctgggtgt ggagtttctg 120

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ctcctctccc	cggtaggagc	ccagcaggcc	acggagcatt	gcctgaagcc	gtggctgggtg	180
ggcctgggtg	cggtagtcgg	cttcctgttc	atcgtctatt	tggctctgct	ggccaaccgc	240
ctctgggtgt	ccaaggccag	ggctgaggac	gaggaggaga	ccacgttcag	aatggagtcc	300
aacctatacc	aggaccagag	tgaagacaag	agagagaaga	aagaggccaa	ggagaaagaa	360
gagaagagga	agaaggagaa	aaagacagca	aaggaaaggag	agagcaactt	gggactggat	420
ctggaggaaa	aagagcccgg	agaccatgag	agagcaaaga	gcacagtcat	gtgaagattc	480
ctggctgcct	cttcaggca	gtccccaga	gatgcctctt	ctgcccccta	aaagcagtgc	540
cctggacttg	aagcccgtga	aatgactcca	tctgggattc	agaatacagt	gttctcaagt	600
gaagaaggct	tggaaaccac	cccactccc	tcattggggg	ctctctgggc	aaacatgggt	660
ttcatgcacc	cctcttctctg	agcttgggtc	ctgcctgggtg	attcttctta	tactcggaga	720
gcacccctgg	ttgaggagac	acccgcaatc	ctccacgac	tcattgggtcc	acctgcttct	780
ccccactgcc	tgatttcttt	tctctctgcc	tgatgtctac	tgaacagaac	ttcccccttc	840
ccatgcaccc	actgccagct	gagagctgct	tcccaatggc	ctgcattaaa	gcattcgtaa	900
cagccaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	tcga	954

<210> 38

<211> 890

<212> DNA

<213> Homo sapiens

<400> 38

aattcggcac	gagattcact	aaacactgca	atacaagctt	ggcaacagaa	caaatgccct	60
gaggtagagg	agttgtctt	cagccatctt	gtgatctgta	atgacacaca	ggagacactg	120
cggtttgccc	aggtggatc	tgatgaaaat	attctgctgg	cgagtctcca	cagtcaccag	180
tacagctggc	gctctcaca	atccccacag	ctgttacaca	tctgtattga	aggttggggc	240
aactggcggt	ggtcagagcc	tttcagtgtg	gaccatgccg	ggacttttat	tagaacaatt	300
cagtacaggg	gtcgaactgc	ttctctcatc	atcaagggtc	agcaactcaa	tggagtacaa	360
aaacagatta	tcattctgtg	aagacagatc	atctgtagtt	acttgtctca	aagcatagaa	420
ctaaaagtgc	ttcagcatta	cattgggtcaa	gatggacaag	ctgtagtctg	ggaacatttt	480
gactgcctca	cagccaaaca	gaaattgcct	tcgtacatac	tagaaaacaa	tgaactgacg	540
gagctgtgtg	tgaaggccaa	aggagatgaa	gactgggtcaa	gagatgtgtg	cctggaatcc	600
aaagcccctg	agtacagcat	tgtcattcag	gtgccatctt	caaacagttc	cattatttat	660
gtctgggtgca	cagttttgac	tttagaacc	aactctcaag	tgcaacaacg	aatgattgtg	720
ttcagccctc	tttttatcat	gaggagtcac	cttcagacc	ccattatcat	acatttggag	780
aaaaggagtc	tgggattgag	tgaacacaa	attattccag	gaaaagggca	ggaaaaacca	840
ctgcaaaaaca	cagaacctga	ccttgtacat	cacctgacat	tccaagcaag		890

<210> 39

<211> 1070

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (1016)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (1026)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (1043)

<223> n equals a,t,g, or c

<400> 39

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gtttataagt	ggttcctgct	aatctataaa	atcagctatg	ccactggcat	tggtggctac	120
atggctgtca	tgttaccct	ctttggtctt	aacttattat	tcaagatcaa	accagaagat	180
gccatggact	ttggcatctc	ccttctcttc	tatggcctct	actatggagt	tctggaacgg	240
gactttgcag	aaatgtgtgc	agactacatg	gcatctacca	targgttcta	sagcgagtcg	300
ggcatgccta	ccaaacatct	ttcagacagt	ktgtgtgctk	tktgtgggca	gcagatcttt	360
gtggacgtca	tgaagagggg	atcattgaga	acacgtatag	gctgtcctgc	aatcatgtct	420
tccacgagtt	ctgcatccgt	ggctggtgca	tcgtgggaaa	gaagcaaacg	tgccctact	480
gcaaagagaa	ggtagacctc	aagaggatgt	tcagcaatcc	ctgggagagg	cctcacgtca	540
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gtgtagtcca	aggcatcaac	tacatcctgg	gcctggaata	gtgatgaaga	gcacagtggt	660
aaaacccacc	ccacacgcca	tggacctcag	ggcactctcc	tccctgcccc	caaagacctc	720
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aaaagaaaac	tattttgatg	aatatatatta	aaaaaccttt	ttttattgtg	gagcatagga	900
attgcccccc	tccaggcttc	accctccctg	cctaagcagg	ttgggggcag	agccatgaca	960
tttttggttt	aaaggagcct	tctcatctct	ggccgagaac	actgctgggc	tcccangtag	1020
ctgaangcct	cagcccaycc	atncccttct	tccctgtgtg	gggtcaagc		1070

<210> 40

<211> 772

<212> DNA

<213> Homo sapiens

<400> 40

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caacaaaaga	gagcatctct	tctcatgaag	gctacactca	aattattgcc	aacgatcgtg	120
gtcatctact	gccttctgtg	ccccgttcca	aggcaaatcc	ttggggttcc	ttcatgggca	180
cctggcaaat	gcctctgaag	atacccctg	ctcgggtgac	cctgacctcc	cgtacaactg	240
ctggtgctgc	ctccctcacc	aaatggatac	agaaaaatcc	tgatttactc	caaggcctcc	300
aatgggctgt	gtcctgaaat	cttaggcaag	ccccatgac	cagacagtca	gaagaaactc	360
agaaagaagt	ctatcacaaa	gactgtacaa	caagcacgaa	gtccaaccat	attccaagct	420
ccccagctgc	caacctcaat	tcccagatg	aactccaaag	ctcacamccc	tctgcaggtc	480
atactccagg	tcccaaaga	ccagccaaat	yctaagagcc	cacctggrag	tccacgtatg	540
ctagaactct	gggcagggcc	taatctagct	gagggtccaga	aatacaaac	tggaacttca	600
tatggaccaa	gtggccacac	actgaaaaac	ccgtatagcg	actcagtga	ataaacaaga	660
gccccagtc	agaactgtga	aacagggaaa	ttttggggtg	gsagtaaaag	saaatttgga	720
aaataaactt	ttttttgttg	aatcttttaa	aaaaaaaaaa	aaaaaactcg	ta	772

<210> 41

<211> 787

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (444)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (506)

<223> n equals a,t,g, or c

<400> 41

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cacctacagt cttgggtcagc agccccactg agctgtgttc atgttgactt ccagctccaa	120
ccttatctcc tgggtcctgc cagagttgtc ctctctgttg tgggttttct tgttctggaa	180
aaggcagtggt ggtgactggg cgggccggaa gaccagggtcc agggctctcag gagttgtcac	240
taatttccca ctccattccc cttcactccg ttacagctcc tttttggaat gaggggacga	300
tgctcaggaa gagaggaggt attggaaagg aaagagaccc cttcatcttc ctttttagcc	360
ctgctcaacc tggctggcta tttctgggag ggcccttttag agttgctgtg ggccctctgcc	420
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ttatttttta ttttgagaca gagtcttgct ctgtccccc aagttggagt caatggcatg	600
atcttggttc actgctacct ccaatcctgg atttgagcta ctcaggaggc tgaggtcagg	660
ggaatcgctg gaacgcggga ggcgagctt gcagtggagc gagatcatgt cactgccctc	720
cagcctgggc gacacagtga gactccatct caaaaaaaaa aaaaaaaaaa aaaaaaaaaa	780
actcgta	787

<210> 42

<211> 652

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (392)

<223> n equals a,t,g, or c

<400> 42

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tacgttgggg agtgccagat gtcaccatct ttcgttcttc ctctggggct ggtcaaatec	120
ccctgagaaa actcctcttg cctcctggcg ggggggtgaag gccaggctgc caggggcagg	180
ctgccagctt ctgggagctg caggggcaga ggcaggagc tgtcaggcat tcagccagca	240
agacgcactc agtaccactc tgggggttcag aatccccctc cctcatcttc agatgggcca	300
gatgtcccca aagccagcgg cccctttctg tttcacctg tctacagaat aaacccccag	360
tcactggggg tgggggaaga gtaaggggag angggaaacg agatttggag gtctagctgc	420
tgctgaaaca gccctcagtt cgtctttatt ttgccttctg caaaactggc ctgggtgttg	480
cagctccttt tgaggacttt gctamcggtt ctcagcatcc ctcaattgct ggcttaggat	540
tcattgggttt ttaggggttg ggtgggatta gcatgtccag ctgctttcca gtttccaaag	600
ttctgtccct atcatattgc ctctgattta aaaaaaaaaa aaaaaaaactc ga	652

<210> 43

<211> 1520

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (799)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (928)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (937)
 <223> n equals a,t,g, or c

<220>
 <221> SITE
 <222> (945)
 <223> n equals a,t,g, or c

<220>
 <221> SITE
 <222> (974)
 <223> n equals a,t,g, or c

<220>
 <221> SITE
 <222> (1019)
 <223> n equals a,t,g, or c

<400> 43
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 gggagtggtta attactttac agggaggtat ggggccatgg tgtttgactc ttctttcaac 120
 cacttctggg ttttttagtg aaaacctcta tctaactctg atactttcat ttctgtgtgc 180
 tattgagtca gttaactctg atccatttat ttttcagttc ccaaaatctt gctttgccat 240
 tgcttctatt ttattgtctg ggggtgttta acacctgttt gcatttttta cagtcattta 300
 gtttccagat tttagtaagg gacagaggga atagatggac tcattcatga tgtagaaaca 360
 aatactccct gtcttgtctt acakgaaaaa ttattcttaa actagcctgt cttkgagaac 420
 ctgatcaaaag tataaaaaat actttttggc ttatttctta gtgagtcamt attccatatt 480
 ttgaagggtg taagaggtat ggtaaagggtg gtacttgaac atttccaagc aaacgtgtga 540
 tgaaatctty catcaatgtc ttagcaatgg tatatgattt ttttagtctt agcaatttta 600
 gataagtttt ttttttgtct tgtttttttg agacggagtc ttgctctgtc gcctaggcta 660
 cagtgtagtg gcgtgatctc ggctcactgc agcctctgcc tccgagcggg gtccagcgat 720
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 atttttgtat ttttagtana gacagggttt caccatcttg gcctgactgg tcccgaactg 840
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 tgctgtggcct gagcactwag ggcgcaanga raagccngta ctgggnawtwt tacactactc 960
 rgcacargac mgnntttaat ctttttcttg ggggacaaga ttggaaaatt gaggtctgna 1020
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 tgtttggaat tgacgttttag ctgtgttcct cactcagata cgtgcatgat agctgcttgc 1140
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 atcccactgt tgctaactctg tctgcctcat aatttccatg agattgagca tcttgttgtg 1260
 tttgtcacca ctatataaca gcatgttgga aacaaagcag taataaagct agaaaaacca 1320
 agcgaataca ctggattaaa aaaaatactg tttcctagaa ttaaagaaat aaatgaggcc 1380
 gggcgagtg gtgcctgtaa tcccagcagt ttgggaggct gaggctagtg gatcatgtgg 1440
 ccgagatcgc gtcactgcac tccagtctag caacagagcg ataccttgtt tcttacttaa 1500
 aaaaaaaaaa aaaaactcga 1520

<210> 44
 <211> 796
 <212> DNA
 <213> Homo sapiens

<400> 44
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 gaccargtag agtgatgggt tgtacagcac tgttactcct tttccatctc tgtgtcccat 180
 gtgaacctta tggcacccat gagaaggagc ttgtaccagg tttatacttt ctagtttaca 240
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aaagtgcaca	ttctttcttt	cttggagaga	aggtggagac	aggtctcac	tctatcacac	480
aggctggagt	gcagtggctc	aatcatggct	cactgcagcc	tcaatctcct	gggtcaagt	540
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gctaattttt	aaagtttttt	gtagagacag	ggtctcacta	tattgtgcat	tctgggtctg	660
aactcctggg	cccaagtgat	cttcctgcct	cggctttcca	aagtgcctga	attacaggca	720
tcacccccat	gcctagcctg	aaaattcttt	ctatgtcctt	aacatcttct	ttcccagtat	780
ttctccatcc	actcga					796

<210> 45

<211> 1378

<212> DNA

<213> Homo sapiens

<400> 45

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ggtatagggt	tggtgcaaat	ggttatttaa	tcttgactag	gtgagaagtc	atagaaattc	120
tcctaatttc	aacatctatt	tattcatgga	tctatattat	ttttgtgtgg	gagaaaaact	180
tttctattta	aagataattt	acaaacgata	ataatctctt	ttaggtatgt	ctattttttac	240
ttgtcaaaaa	cacataacat	ttacaatagg	atattttgaa	atgtttattt	tagtcctatt	300
atattgacat	tggtatgcaa	catattccka	aaakgttttk	gtcttgcaar	gctaaatatc	360
aatacccat	aaaaaactat	ggaattttac	ccatttccctg	ggcacttttc	aaacaccact	420
ctgttttctc	taagagtgtg	ctggcttcat	atatctcata	caatctctgt	ctttttgtga	480
ctggctcatt	ttattttgca	caatatcatc	aagctttata	gttggttagaa	tattttctgc	540
tttttaaaaa	ctgggtgata	tttaagtatt	ttgtatttta	gattatatct	actgagtaat	600
ttggkgacaa	atttgcackg	cttttaccta	ttggctttca	gtaacaatgc	tgcaataatk	660
acmggtatgc	aatgaccta	tatgatcata	tatgtgtaag	tttatatatg	tgccgcattc	720
tgttctacta	gtgtacgttt	ttacctttgt	actcatacca	aattgttaca	attctgtagc	780
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agcaggatgg	acatcttcac	aagattaatt	attttaacat	ttcaacaagc	atgctcaaga	1020
gtgtattgtt	ttattttcta	tgtattttgt	aatttttcag	ttttttcttc	ttactgttct	1080
atactcattt	cattttgggt	atataaagta	atccataaaa	atttagtttt	aaataatttg	1140
ttaaagactc	ttttttgggt	taccagggtt	tctatcaagg	agaatttcgt	atgagggtatt	1200
tagaaggctg	tttatcatta	tgttgttgag	tggtctttat	gcctctgtta	ttaataattg	1260
ttttatactc	ccttcaagtc	cggtttcttt	accaatattt	tgtcttttta	aaatctttat	1320
tacagaaagt	gaagcattaa	aatattctac	tataaaaaaa	aaaaaaaaaa	aaactcga	1378

<210> 46

<211> 597

<212> DNA

<213> Homo sapiens

<400> 46

tggcgccgc	tctagaacta	gtggatcccc	cgggctgcag	gaattcggca	cgagcccggc	60
cgccatcttg	ggtcatcgat	gagcctcgcc	ctgtgcctgg	tcccgcctgt	gaggggaagg	120
cattagaaaa	tgaattgatg	tggtccttaa	aggatgggca	ggaaaacaga	tcctgttgtg	180
gatatttatt	tgaacgggwt	tacagatttg	aaatgaagtc	acaaagttag	cattaccaat	240
gagaggaaaa	cagacgagaa	aatcttgatg	gcttcacaag	acatgcaaca	aacaaaatgg	300
aatactgtga	tgacatgagg	cagccaagct	ggggaggaga	taaccacggg	gcagagggtc	360
aggattcttg	ccctgctgcc	taaactgtgc	gttcataacc	aaatcatttc	atatttctaa	420
ccctcaaaa	aaagctgttg	taatatctga	tctctacggg	tccttctggg	cccaacattc	480
tccatatatc	cagccacact	cattttta	atttagttcc	cagatctgta	ctgtgacctt	540
tctacactgt	agaataacat	tactcatttc	gttcaaaaaa	aaaaaaaaaa	aactcga	597

<210> 47
<211> 600
<212> DNA
<213> Homo sapiens

<400> 47
agaactagtg atccccggg ctgcaggaat tcggcacgag gacctctgac catcaggctt 60
ctgggaacca taggctatac ccacaccaca gagcatcgat aaactatatt gatgtttctc 120
ttgctttcag aaagacagct tccaagattc aagcccaggt ggtgccggtc tttttttgga 180
ggtgctaatt aataatttaa ctcatctaa tgataatttt atcttggtgc agtttgtgga 240
tttatgatta tctcatccat ccggtgccta gtgttgggca tagagtgtgt ctctgctgtc 300
tgccagaatc tgctactggg agaatttccc cactgggaga gggaccagga aaatggcatg 360
gtcttagaag gtctcctgaa cacatttccct tgggagggct cctgttatct tcaaggttga 420
tggctttctg caatctctca agggctgttt tgcctggaaa caggacgatg gagacagaga 480
cctatcagct gtgggcatct caatatcagc ggaatgggt atcaagaagt ctccagccagg 540
tgcagtgcct gcgcctgtaa tcccaacact ttgggaggct gaggtaggta gatcactcga 600

<210> 48
<211> 911
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (6)
<223> n equals a,t,g, or c

<400> 48
cccgcnngta aagggaacaa aatcgtggag cgccaccggs ggtggcggcc rcgtctagaa 60
ctagtggatc ccccgggctg caggaattcg gcacgagcac ctatccacct tggatcgtag 120
cgtgatatgg tctaaatcta tactgaatgc gcgttgcaag atatgtcgaa agaaaggcga 180
tgctgaaaac atggttcttt gtgatggctg tgataggggt catcacacct actgtgttcg 240
accaaagctc aagactgtgc ctgaaggaga ctggttttgt ccagaatgtc gaccaaagca 300
acgttctaga agactctcct ctagacagag accatccttg gaaagtgtatg aagatgtgga 360
agacagtatg ggaggtagg atgatgaagt tgatggcgat gaagaagaag gtcaaagtga 420
ggaggaagag tatgaggtag aacaagrtga agatgactct cmagaagagg amgaagtcag 480
gtmagtccta amatgcaata aaatgagtca gtaagtctta gttagacaat ttctccacta 540
ttcaaataca aatggaatag ttagggctctg taacttagtt taaaactaat atataggctg 600
gacacggtag cttatgccta taatcccagc actttgggag gctgaggcag gcagatcacc 660
tgagggtcagg agttcgagat cagcctggcc aacatggtga aaccccgctc ctactaaaaa 720
ttgaaaaatt agccaagggtg ttggtggaca tctgtaatcc cagctactcg ggaggctgag 780
gtaggagagc tgcttgaacc cgggagcgga gggtgcagtg aggtaacgga tcacgcmtat 840
gcactycagt ctgggtgaca agagcgagac tccatctcaa aaaaaaaaaa aaaaaaaaaa 900
aaaaaactcg a 911

<210> 49
<211> 1863
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (172)
<223> n equals a,t,g, or c

<220>
 <221> SITE
 <222> (1820)
 <223> n equals a,t,g, or c

<220>
 <221> SITE
 <222> (1826)
 <223> n equals a,t,g, or c

<220>
 <221> SITE
 <222> (1833)
 <223> n equals a,t,g, or c

<400> 49
 gaattcggca cgaggatgat atggacatat gtagcccagt ggcattgtac tttctgcga 60
 cagctgcaca cattacagct gtctccaaac ccacagtgat gcttagggaa agaccctgct 120
 caggaccag caggtcagca ccccagagca gactgatagg tccgtgggac cnatgttaga 180
 gcagaaaatt tgggctcagc acattttact gttagtagag agccaggaaa cgttttcgg 240
 gttggggatt ttgtgggatt ttttaatttt tttagtaggt tttgtttaac ctctgtgcag 300
 tttgtatgaa tgaattgcta tacatttata aggagccagg gtctggagggt ttgctatcac 360
 tttgtccagc ccaaatacct tcctgggcaa ctctaccat ttgtttgcag ttgcctctac 420
 tagctgatgg cagtatgctg gaaagaggtt gtactataaa gagagtctt tccttctact 480
 ccagagttgt tgtgtagctt tgccattgaa ccgatcaatt tttaaactct ttaaagaagc 540
 agcctggcca acatagtga gccccgtctc tactaaaaat acaaaaaatt agctgggcat 600
 ggtggtgggc gcctgtagtc ccggctgctt gagaggtcga ggcaggagaa tcgcttgaac 660
 ctgggagtg aggttgcggg gagccgagat tgcaccattg tattccacc cgggtgacag 720
 tgcaagactc catctcaaaa aaaaaaaaaa aatttggcat catttacaat ttcatagaat 780
 tactgtgaag gcctttctag ttgagatgtt ggggtatttg ggattctaatt tgttaacccc 840
 agaagaaggt aatttagctt gtatttattt aaaaccatt tagcctttta cttatatctg 900
 gtagaattcc agtgatcatc ctaataaggt atatttcaga ataatttttt tttccttcag 960
 aataacttag aatcagatgc tataagggtt cctaggagca gtgtgaaatt tccgtaaaga 1020
 taaatttgaa tgttgtaacc aagtttata taaaccaaga ggccatttcc aatatgattt 1080
 tttgtttctt ttttaactgt taagtccta agagattaca tgctagggtt tgagtcattt 1140
 ctattgtaga taatgatggc ccacacagtc accttcaact atccacataa gctaggcttt 1200
 ccgcttttgc caccgacagt gtgaccaaga tatttcaga gtaaataacc caccacaacc 1260
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 catgtggtga ccccatattt ttctgaggtt ctcttttcc atggtgttac tttattarca 1440
 gaaagtaaat tcagaaaaca ggtcttgccc ttagcagaca agaaccacac cagtttcttg 1500
 taaaggtaac ggatacattg ggattcagga gtgacacaga ggtccagccc cagaacttgt 1560
 aaggattttg tttgaacact gagcagatgc ctctccctg ccaccatca cactagttag 1620
 ggctggccat gaattctatg ccagagtcac tcctgcagtc tgctagggat gggccttctt 1680
 atcccactct cgcacacatc ccagtcagtc ctttgccttc acagagtcct ccttgacacc 1740
 cctgacttaa tgatagttgc tgttttgag tagrattgat caggtttaag tcatcctgct 1800
 caggttgggg catagtgggn tcatgnctgt tantttcagg catttgggga agccaaagtg 1860
 gaa

<210> 50
 <211> 810
 <212> DNA
 <213> Homo sapiens

<220>
 <221> SITE

<222> (688)

<223> n equals a,t,g, or c

<400> 50

gatectccac	atccttccat	ggctctgaag	aataaattca	gttgtttatg	gatcttgggt	60
ctgtgtttgg	tagccactac	atcttccaaa	atcccatcca	tcaactgacc	acactttata	120
gacaactgca	tagaagccca	caacgaatgg	cgtggcaaag	tcaaccctcc	cgcgcccgac	180
atgaaataca	tgatttgga	taaaggttta	gcaaagatgg	ctaaagcatg	gggcaaacca	240
gtgcaaattt	gaacataatg	actgtttgga	taaatcatat	aaatgctatg	cagctttkga	300
awawgttga	gaaaatatct	ggttagggtg	aataaagtca	ttcacacca	gacatgccat	360
tacggcttgg	tataatgaaa	cccaatttta	tgattttgat	agtctatcat	gctccagagt	420
ctgtggccat	tatacacagt	tagtttgggc	caattcattt	tatgtcggtk	gtgcarttgc	480
aatgtgtcct	aaccttgggg	gagcttcaac	tgcaatattt	gtatgcaact	acggacctgc	540
aggaaatttt	gcaaatatgc	ctccttacgt	aagaggagaa	tcttgctctc	tctgctcaa	600
agaagagaaa	tgtgtaaaga	acctctgcaa	aaatccattt	ctgaagccaa	cggggagagc	660
acctcagcag	acagccttta	atccatttca	gcttaggttt	tcttcttctg	agaatctttt	720
aatgtcattt	atatacaaaa	gaaattctca	aatgttaaaa	taaaggaata	gtttattgct	780
taaaaaaaaa	aaaaaaaaaa	aaaaactcga				810

<210> 51

<211> 956

<212> DNA

<213> Homo sapiens

<400> 51

aattcggcac	gagctaaagc	atggtttcca	agatgctaca	ggcagcgagc	ctctctctag	60
tgacctgggt	agtttgcacg	gtttggctgg	aaaccacagt	cccccatct	ctgccagaac	120
cccccatgtg	gccactgtcc	tcagacagct	cctggagctt	gtggataagc	actggaatgg	180
ctccggctcc	ctcctcctca	acaagaagtt	tctcggctct	gcccagagatt	tgcttctgtc	240
tttggtagtc	ccggstcctt	ctcagccgag	gtgttgctca	catcctgaag	acacgatgaa	300
agcattctgc	aggagggagc	ttgaactgaa	ggaggctgcg	cactggctcc	taatgacatg	360
gaaagtttga	agcaaaaact	ggtcagagtg	ctggaggaaa	acctcatttt	gtcagaaaaa	420
attcaacagt	tggaggaagg	tgctgccatc	tcaattgtga	gtgggcaaca	gtcacatact	480
tatgatgatk	ttctgcacaa	aaaccaacag	ctgaccatgc	aggtggcttg	cctgaaccag	540
gagcttgccc	agctgaaaaa	gctggagaag	acagttgcca	ttctccatga	aagtcagaga	600
tccctgggtg	taactaatga	gtatctgtcg	cagcagctga	ataaggagcc	aaaagggttat	660
tccgggaaag	cgctcctgcc	tcctgagaag	ggtcatcatc	tggggagatc	atcgcccttt	720
gggaaaagca	cgttgtcttc	ctcctcacca	gtggcacatg	agactgggtca	gtatctaata	780
cagagcgtct	tggatgtctc	cccagagcct	ggcttataga	gctagcatgg	aactcacacc	840
acagcttccc	tgggtccacag	aggstctcac	cgccattgca	ccagtatgg	ggtatgtact	900
cacaaagatt	aagaaagaaa	tgtattctga	ytataaaaaa	aaaaaaaaaa	actcga	956

<210> 52

<211> 300

<212> DNA

<213> Homo sapiens

<400> 52

gaccatatgt	tgaggaagt	caaactggac	tttttgtggc	tactaaattt	gcctttaatc	60
ttattgttct	caattttgga	atcaagtatg	aaaatctgca	caaatgcaat	gtttacaaga	120
actggttgat	tctgggaggc	atctgtctaca	gtctcttttt	atatggatat	gtacatgtcc	180
tattctacaa	aaatgattaa	agataaaaaa	atacttgat	cccactgcta	ctttagctgt	240
caaatttggt	gtttcatcac	attaaaagca	ataaatcagt	agttggtaat	gtataaaaaa	300

<210> 53

<211> 841
 <212> DNA
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (836)
 <223> n equals a,t,g, or c

<400> 53
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 gctcatagtc ctaaggatct ccagcaccct gccgggtggca ctactgagag acgaggtgcc 120
 aggggtggttc ctgaaartgc ctgagcccca acttatcagc aaggagctca tcatgctgac 180
 agaagtcacg gaggtctggc atggcttagt gatcgcggtg gtgtccctct tcctgcaggc 240
 ctgcttcctc accgccatca actacctgct cagcaggcac atgggtaact ggctcagcat 300
 cctcttccct cctagtcact ctcagagacc attctcgagc ctccagcagg acagaccctt 360
 tggagtcccc aaacgtcact caaaaactac cagaggaccc accggccaaa ttccttccca 420
 ccgctccccc tcccccaat aactgtatct gggtaatccc cactctgacc tcacctttta 480
 accaactatt tctggctgga agtggccatc cacatccgct tactaccag accttctgcc 540
 tagacacagc ttttgcaatg tcctacgagg aagtgcctgt gtaacctggt ctaattaatt 600
 ttcttcatcc ctgttaaagg actgaatatg aagaaatgtc cttgaattac aacagaagga 660
 aatatgggtg gacttagaga ttagtttaaa ttcttgaact gataaacaat agaaggtag 720
 gaagctcggg cctggaaagg catttcaatt agggaaaata aaacaatgct gctttgggtg 780
 tgctaagaaa aaaaaaaaaa aaaaaaaact cgtagggggg gtcttggtac ccaatngtcc 840
 t 841

<210> 54
 <211> 634
 <212> DNA
 <213> Homo sapiens

<400> 54
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 tactcctcgt ctagcttcac tgaatggcag agcccatagc ttgtctttgc ctaatctgct 120
 gcataatcat ttcagcaaca actcaaatgc cttttgaggg ttcttgcttc tgtttggtgc 180
 cttgtaattt tcaaccatat tttagacact ttaggcctaa tgatctaagg catatggttt 240
 ttacccatgg tctgtgggcc cttgagaagc tgagtcctct gaaagaaaat cagaatgttg 300
 catgcatctg tatTTTTTgt cttagatttc acttgattct caaatggatc cttgactccc 360
 ccaaagttaa atttattcaa caaatctttt tttctctcca tactttttat tctgaaacat 420
 attcccccaa tttttaactt ctgaaaaatt tcagacaagt tattggaata gggtagtgag 480
 tatctatgaa cctttcatat aggtttactt taaaaaaat acaagagaca gggctctgct 540
 ctgtggccca ggctagagtg ctatgattgt gccactgcag cctgggtgac agaacaagac 600
 cctgtcttta aaaaaaaaaa aaaaaaaact cgta 634

<210> 55
 <211> 863
 <212> DNA
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (7)
 <223> n equals a,t,g, or c

<220>
 <221> SITE

<222> (298)

<223> n equals a,t,g, or c

<400> 55

gggcagnagt	tccatttctg	ccgtgggtccc	agcagcgctcg	ctgtgggtct	ggcctggggtt	60
gcgtgtgttt	cgatgtggg	ccgtgctccc	tgcttggttc	ccttttcctg	gaacgtgtca	120
ctgcctccct	gtctcgctcc	gtggacattt	ctgggaggtc	aggccgtggc	cacctggccc	180
ctgtttcagg	tctgaggctc	ccacctgctt	aggttcggga	agctcaggag	tgaggccatg	240
ccctcctcag	gacatcccat	ccaagccagc	catgtccggt	gatgggccgc	tgcccggnaa	300
agtccttttc	cttcttgtaa	ctgagaagaa	cttgccctga	gccacgtcaa	gtcccgtccg	360
tcgcagccac	tgcccacaag	cgtgagtcctg	ctgtgagcca	gcggctccat	ggcaggggcat	420
cccagcgcca	ttcctgcctt	cacacacact	tgctgccgtt	tcctgtgtct	gggggtgtg	480
cargtctgcc	tcggtgtgga	cttttctctt	aggaaagagc	cccaggtcgg	ccgagcacgg	540
tggtcatgc	ctgtaatccc	agcactttgg	gaggctgagg	cgggcagatc	acgaggccaa	600
gagatcaaga	caatcctggc	caacatgggtg	aaatcccgtc	tctacttttt	aagtatttta	660
tacttaaaat	ttttgtattt	tatacaaaaa	ttagcgggct	tggtggcaga	tgctgtagt	720
cccagctact	cgggaggctg	aggcaggaaa	atcacttgaa	cctgagaggc	ggagattgca	780
gtgagccaag	atggcgctcca	ctgcattcca	gcctgggcga	cagagcaaga	ctctatctca	840
aaaaaaaaa	aaaaaaactc	gta				863

<210> 56

<211> 712

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (20)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (44)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (56)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (128)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (625)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (692)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (699)

<223> n equals a,t,g, or c

<400> 56

tggtgttgg	aattgtggn	cggattaaca	atttcaccac	gggnaaccgg	ctttgnccca	60
tggtattccg	caaggcccga	atttaccct	tcactaaagg	ggaacccaaa	gctggagctc	120
caccgcgntg	gcggccgctc	tagaactagt	ggatcccccg	ggctgcagga	ttcggcacga	180
ggtttcctgt	cagtgtctat	gagattttat	tttattaatg	tctgcactta	gttttacttc	240
ctactttcta	cttttattga	gagttaaacc	tggtgaagtc	tcagggtcaa	ttcctcacc	300
tgagcaacct	aatgttttat	gtctgttct	tcctacattt	ggttattgaa	actgaagttt	360
taggttacca	gatttgatag	aagcacataa	gactacttac	tgctttagtc	tcaattatta	420
attgagaaat	tatcaattaa	caataaggat	ttctcttatt	tttccccaa	ataagttata	480
tatttaagt	gtgttttata	gtagaaagg	tttagaatat	ttgggttgct	acattaattg	540
aaatggcagc	tgaagatgtg	atttcagcc	agggatttat	taaaaaaaaa	aaaaaaaaac	600
tcgagggggg	gccgtacca	atcgnctat	agtgaagtcg	atacaatcac	gggcgtcgtt	660
acacgtcgga	ctggaaacct	gcgtaccact	ancgctgcnc	acacccttc	gc	712

<210> 57

<211> 925

<212> DNA

<213> Homo sapiens

<400> 57

gatttaaatg	tggtgttct	tttataaac	attgaatctg	tggttgggtt	atttctgtca	60
atttatgtgc	cttccttgc	aagtcacact	ttgcctaatt	gatgtcctgt	gtgttttcca	120
ttccgttcat	gctgaattat	cttaggtcaa	agaggaaatc	atctttctgc	ctccaacctt	180
cttacttgcc	tctaattccc	tttcttgact	cttccaagtc	aggattctca	ccaagggaagc	240
tatctgcctt	ctttgggaat	gttgggctta	tgaagacttg	gagataatgg	ggttcatgta	300
ttcagactct	ttrgcatwta	cagtagagtt	tctaattgtg	tcagcattcc	ctagtgggca	360
gttacaagtt	aggttgggat	tctaataata	tttatgatas	tcacagatta	aattgcactt	420
tgctcttgcc	ccagtccttg	attccctttt	ggccagcagt	ttttaggtct	gtcagtactg	480
cactgcarga	atggcagatt	ttgggatctc	tgctggccag	tttgggagc	tggtctggga	540
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tgatatctga	gttttcattt	agggtggcat	gtgatagtgg	tggtctggta	ccctgttggt	780
tttcagttga	gatatatcgg	aggaaccacc	cccaataatt	caacgtaggt	tcttttctat	840
tttccttaag	tgctggctgg	tctgagaaat	aaagggaaag	gatacaaaaa	agaaaaaaat	900
aaaaaaaaaa	aaaaaaaaaa	ctcga				925

<210> 58

<211> 601

<212> DNA

<213> Homo sapiens

<400> 58

gctgccagga	attccggcac	ggggaacagt	gtaatatgta	agcaaatgct	gtataacaac	60
cacctggaag	cccctcatgt	atctcttttt	gaaaacactc	ctctctttct	ccactctaata	120
gatgaccacc	gccttgtctt	ttatggtaat	cactgttctt	tggtttttat	tactgcattt	180
attggctaata	atatgcatcc	ctagaaaatg	tagttttgcc	tgcttttata	taaatggaat	240
attactgcat	gcagtctttt	gatttgtgat	tgttttgtct	taaggcttgt	aagggtcatc	300
catgttttgc	atatagtttg	tttattgtca	ttgccataga	gtaaatcatt	gtatgaatat	360
actgcagttt	atttactgtt	gacatatgtt	tcagttgttt	ttaactacta	ggaaatgcta	420
ctctgtacat	tcttgtatat	gtaccttggt	gcacatatgt	atgtttttct	agagtatata	480
cagtggcatg	ggattgtctg	attaaaagg	ttgtatatct	tatactagaa	gataataaaa	540
acttttctct	atggattctg	ccaattcaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaactcg	600

a 601

<210> 59
 <211> 730
 <212> DNA
 <213> Homo sapiens

<400> 59
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 atgccatctt tttaacatgg tctggaactg aacctacaat atttctgaga aaattgactt 120
 tgcttctttg agaacagcat ggtgagtcta ctatccttga cttttcatca atttgtttca 180
 tcaactaaagt atttcaagtt gctgtctacg tcaaggcaag aaattctgta ggggttcagc 240
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 ttaaatgtgc wctatctgga tccatattct ggcacaatct gcctcttgatg atgaagatga 360
 aaatgggtac cttaaagtgc tcttcgggtc ggccttcttc agtttttagca tctctaataca 420
 ttgcagcaac gtatcgcttc accagggtcc tcataacttc ctgaggcatt ttagaacaag 480
 agtattgata ctcaatgagt aaataaattt cctcctgagt cagtcttgaa ggggggactg 540
 catttttattt tagtgaaaat ttcaagacat agtacaagga caacttactt ggtattgggtg 600
 atgtcttctc aagttatcag cagctcgctt ctgaaaagga aaaggacatt cctttctggt 660
 tatactgtta tattactatt ctaaaaaata atttattttt ttaatcgaaa aaaaaaaaaa 720
 aaaaactcga 730

<210> 60
 <211> 846
 <212> DNA
 <213> Homo sapiens

<400> 60
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 agtttacaca gataatattg agaggcttcc ttgggaattt gaaaggagtc ttcaaatcat 120
 cctttccctc agagatgaaa aaatatttta aaaaaattac tgtcttgat atttgatatt 180
 ttgaaaatgg cagggaatca acaatttgtt aatctgttgt taagatcagt tatacattca 240
 gtggcatact tcttgtctta gaaattggtt gaaattaata ttgctagtga aagtgtggaa 300
 atagraacag ttgaaaggaa gacaaatgag aagtggacct tgcttctcat gaggatgctg 360
 cagaactaga gtggttgccc agcaggatga aaatctcaat taattgcttg acagagaatt 420
 aaaacaaagg caagtgggtc ttttaaaaaa gataaaaaata ggtgaatata aagttgaaag 480
 gaggccaggt acagtggctc acacctgtaa tcccagcact gtgggagccc aaggtgggtg 540
 gatggcctga ggtcaggagt ttgagaccag cctggacaac atggtgaaac gctgtctcta 600
 ctaaaaacac aaaaattact tgggcgtggt ggcatacgcc tgtaatcaca gctactccag 660
 aggctgaggc aggagaatca cttgaacctg gaaggtagag gttgcagtga gccgagatcg 720
 cgyccattac actccagcct gggtgacaag agcaagacta tgtttccaaa aaaaaaaaaa 780
 caactgaata ttggatagag aggagaaaaa gggcaatgta tcaaaaaaaaaa aaaaaaaaaa 840
 ctcgag 846

<210> 61
 <211> 958
 <212> DNA
 <213> Homo sapiens

<400> 61
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 ggttattttg ccatgactgg ctgatcttga gctcaaggat ctgcttcaaa tgcacacagg 180
 cctagtgtgaa gtttaaaccc cagcaaaaaca ttccctccctg taaatggaaa atcctacttc 240
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ccctcctcac	tgctcctct	ctgggacagg	ctgggacctt	gaggaagata	aagccttcct	360
tgactacca	tcatattcag	tgccctgtt	cctcactcag	agaggaggc	agaaccagtc	420
aggcttattt	cagtaagttc	cacagttcta	caagactgca	ggaattctcc	ttaagggagg	480
agagcaagca	ggtgtggccc	cagcttctgg	aatggcaga	agagagggtt	ttctcattga	540
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caactcctgg	gaggagaggg	tctcaagagt	tgccctgga	aggagggcgg	gggcagtcg	660
catctatttc	aggttgtggc	tcttggttct	aggactctta	cttctctggc	taagggctca	720
gcttcttggg	acttcaacca	tcttctttct	gaaagaccaa	atctaattga	accagtaacg	780
tgaggactgc	caagtatggc	tttgtcccta	tgactcagag	gagggtttgt	cgggcaaatt	840
caggtggatg	aagtatgtgt	gtgcgtgtgc	atgggagtgt	gcgtggactg	ggatatcatc	900
tctacagcct	gcaaataaac	cagacaaact	taaaaaaaaa	aaaaaaaaaa	aaaaaaaaa	958

<210> 62

<211> 582

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (20)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (27)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (49)

<223> n equals a,t,g, or c

<400> 62

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tgaggacttt	ggactggcat	aaatcatagg	aatatgatta	tgaggataca	tccaattttc	180
agattgggca	atgtatacag	tttattatca	tttctgattt	tgggtagagt	tagtactaag	240
aacagcattg	aagaaaagca	gtataacatt	aaaattaaga	agatttaaaa	tacaagagga	300
ttcataacag	tcacttttaa	aatattgttt	tggttttcta	ctttggagct	gtaattttta	360
aaaaagaatg	aacagggttt	tgtatgaata	tgtagaatg	actaattata	gagcatcttt	420
caactggaat	acatgtagat	actaacacct	ggttgatttt	gatgtaattt	cagtgcatac	480
agtgtgtgta	atctgtatta	agtgaatac	ttatgaataa	agttgtttct	gcattgcaaa	540
aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaactc	ga		582

<210> 63

<211> 752

<212> DNA

<213> Homo sapiens

<400> 63

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gcacagtgat	tccagagaga	agtctttgct	cctccatcta	tggaactt	tctcacattg	120
tatttattac	tatatgtttc	ttactggagt	gtctctccta	ctggacaggg	agcaggttta	180
tttattgctc	agtccctcagc	ccctggactt	aggcagactc	atagtagaca	tttgggaaat	240
gcttgggaaa	gaaaggaggg	gaggagagag	gaaggactcc	atggccatgt	ctaaatgccc	300
agcaatgtca	tagaggttat	gggggtgcag	gagaagacac	agccctccct	ctggcagcta	360

ggatagagcc	tagctgctgt	taaagacagg	cagctcattc	ctcacctggg	ccaagctgca	420
gctggtcatc	tctgcccctt	tctccttcca	tcttatggga	gcttttatgg	agtcagaagt	480
gagtgaggca	gacctgggag	agccctacac	tcaggaagaa	tgtaggctgc	agaaaggaac	540
aggtgtcctg	gagttagctc	aggaaggtct	tgaaggaagg	ggttaacyag	cagatggcaa	600
cccagtgact	tttgttgctc	tctgaagcca	cagaggaaaa	cagtagcaac	rrratraaat	660
aaaataaaat	aaaaaataat	aaaaaagcaa	agttcccaag	gaaataagat	gggggaattc	720
gatatcaagc	ttatcgatac	cgtcgacctc	ga			752

<210> 64

<211> 706

<212> DNA

<213> Homo sapiens

<400> 64

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tcaaaaacac	tgagctcctt	ttcactgtgg	ggccattgaa	tatgctgttt	tccctcccta	180
gaaccttttc	ctctcattct	tcacctgccc	aactcatatt	tatccatgca	gcctcagttt	240
taatggcatt	tctctcccagg	ccttccaaga	ccactctccc	tcaggcagct	ttcctgacat	300
cttttagcctg	cccgtcatg	ctctctacct	tttttctgta	tcaaaatgcc	tttgtttgca	360
agtaacagaa	ggcctgactt	aacctgcctt	taaacagtaa	ggacacaagt	atgcctatgt	420
tatttagaggt	ctgcaggtaa	ggcacgtaaa	gggtcatctt	tttccagtgt	cttcaactcc	480
atttctctga	ggttccatca	gctacattct	gtgccatgac	tttatcctca	gtgcattttt	540
cagatggtaa	tcaaatggct	gtaacatgtt	cacctctagc	tcagcatgat	actcagagga	600
agaatagagt	tgcttctagg	agttttgtga	tgagaatgag	ggaatttctt	tccctggagc	660
ctccagcaag	cttgtcatta	agtacctcct	cagggtttctg	gctcga		706

<210> 65

<211> 400

<212> DNA

<213> Homo sapiens

<400> 65

tcgaccacag	cgtccgccct	gcatggcgag	atgtcctcct	ttcccggggc	acagtgtgtg	60
caactaataa	acctcctcca	tctcatctgc	ccagtgtcgg	gtcttggtgtg	ttcagccatc	120
accatagccc	tcaggcagaa	gtccatccct	caccaacagg	gaagagaggg	agtgatcaaa	180
acacctcctc	caggaagtct	tccctgaagt	tcgtagtctg	gcttcagtgc	cacttcttcc	240
ctgccctcat	attcgctaac	cgccacttac	tgcttggttt	tcagcctcac	taggatgtgg	300
gccactaagg	gccaacatgg	tctactttgc	agctgcatta	tcagggccta	ccataacacc	360
ttccaaatgc	ttaaaaaaaa	aaaaaaaaaa	aaggggcgggc			400

<210> 66

<211> 773

<212> DNA

<213> Homo sapiens

<400> 66

gcacaggat	gttttctgat	ggcacaggcg	aggtcacaga	aaagtggatg	gcaggcggtg	60
ctgtctgtca	gaataacacg	aaagtgagag	aaggccgctc	tttcagaata	acaccacaag	120
tgggagaagg	ccgctccctc	agggctggcc	atgaataaat	ggggatttct	gcctgttytc	180
tccctcccg	ctcactccct	tttctgcag	aggcagctcc	tgagccattg	ccgagcagga	240
tgctagtgtt	agcatggatt	acatttccac	cgtgtaaagc	ctgctgcatg	atgtgcatct	300
tctccagccg	cctccttcag	caggagargg	tttgacart	tgtccaggga	arggaacctt	360
ggggcatggc	ccaacgggac	agaggatttg	artccctctg	attatgagca	gggttaattt	420
aaagtgaaaa	ccatggttac	ccattgccct	ttaaaaamca	cccagggggc	gggcacagtg	480

gctcatgcct	gtaattccca	gcacttttgg	aggccgaggc	aggcagatca	caaggtcagg	540
agatggagac	catcctggct	aacatgggtga	aaccccgctct	ctactaaaaa	agtacaaaaa	600
attagccagg	cgtaggtggcg	ggccgagtag	ccccagctgc	tcgagaggct	gaggcaggag	660
aatggcgctga	acctgggagg	cggagcttgc	agtgagccta	gatcgcgcca	ctgcactcca	720
gcctgggtga	cagagcaaga	ctccatctca	aaaaaaaaaa	aaaaaaactc	gta	773

<210> 67

<211> 647

<212> DNA

<213> Homo sapiens

<400> 67

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ttaacaagtt	tgagatcttg	ttatatattt	tcatttggtg	ctttataacc	atttctctat	120
attactaagt	ttaattaagg	tctggaattt	ttttagatgg	tgtatcatgg	gtataatatt	180
tatttagttg	ttttcctctt	gttatatatta	gattgaggca	gtgctacagg	ctttaactag	240
agaggtggtt	ggctgttcag	gactgggagg	tggaggacta	gcaggaacag	aggatatagca	300
ggagagcatg	cctactatgg	gtataggggc	agtaaggaga	gcagctgaag	cagccacca	360
ttaagaaagc	gttcaagctc	aacaccact	acctaataaa	tcccaaact	ataactgaac	420
tcctcacacc	caattggacc	aatctatcac	cctatagaag	aactaatgtt	agtataagta	480
acatgaaaac	attctcctcc	gcataagcct	gcgtcagatt	aaaacactga	actgacaatt	540
aacagcccaa	tatctacaat	caaccaacaa	gtcattatta	ccctcactgt	caaccaaca	600
caggcatgct	cataaggaaa	ggttaaaaaa	aaaaaaaaaa	aactcga		647

<210> 68

<211> 675

<212> DNA

<213> Homo sapiens

<400> 68

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gcttggttcc	tgtttaagga	gatggggcca	gcagtgtgtt	tcagggcctg	tgaaatgtgt	120
tctctatccg	ggcttttgc	taatctctgt	tttcagtctt	gcctatcagt	cccactgtcg	180
ggggtacctc	gtgtctgagt	ctagaacctt	tccagggtgc	tgtgggacag	attagcctcc	240
ttgttctcag	tatccctga	cctccacctt	tattgctttg	ctccatgaat	taaccatttc	300
catgtactgt	catgtcta	gaagatgaat	tctctctgt	tggtaaaccc	attccttttt	360
tgtaattgtg	tgcttataca	atgtttattc	ttcactgtat	ttctattgga	gcctcaggac	420
aaagagcaga	tggtgagaat	ctgtgttcag	tgtaagttt	tccttctgta	agacatgtgc	480
aacttgtgtt	tttactgaa	tagatcatgg	acttaatgca	tatagagcta	ctttgttttt	540
catgattgtg	ccttcaatta	tatgtagaaa	tataatttgt	gaattgcctg	atgaaatttt	600
cctaattttg	aattatcttt	gcattcctat	aataaacact	gttagaatgg	caaaaaaaaa	660
aaaaaaaaaa	ctcga					675

<210> 69

<211> 889

<212> DNA

<213> Homo sapiens

<400> 69

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ttagcccatg	aacttgagga	cagttttgct	gagcagaact	tcactctctg	gctttgctgt	120
ttgtttgcct	tgtttttttt	gttggtttta	cttagttttg	tttttgagac	taacatccat	180
aacttttgct	atgtatgata	taatccccctg	tatgaccctg	ggcaagtaac	ttaaccatt	240
cagggtccag	gttcctctta	tgggaaagg	atgcttgata	agacactgtt	catggttctc	300
tgcagtttac	tattatgata	gatattcgat	gacctaaaaa	ttaaaccagt	ttcctttttc	360

aaattttaatt	tttycgggag	gtggaggaag	attttcattc	cttatggttt	gagaaacatc	420
gctttcatac	atgtctaggg	taaccaagtt	ctctaataa	tggcaatagt	gatgtatttt	480
yctwaaatcc	ttttctaamc	agcattatgg	gtttgtgctg	taccggacaa	cacttcctca	540
agattgcagc	aaccagcac	ctctctcttc	accctcaat	ggagtccacg	atcgagcata	600
tgttgctgtg	gatggggtaa	gaatcgcttc	tgaactgtgc	ctggcttttc	tccactatct	660
tgaatcaga	tgggaggagg	cttttttctg	ggtgggactg	aggaggcaca	ctgaagtccc	720
ccaggtcatc	ggggctgggc	cattgccttt	ttccccacc	tgggtagtcg	tggacagaag	780
cttgggatgg	gatggagagg	agagatcgtg	ctgtgtgtca	tgtctgttgt	tcaagtaaat	840
aaaagtgtgc	ctgacttcaa	aaaaaaaaa	aaaaaaaaa	aaaactcga		889

<210> 70

<211> 888

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (347)

<223> n equals a,t,g, or c

<400> 70

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aataattatt	taaaaaacca	cacacaccag	aaaaacaaaa	gacagcagaa	aataaccagg	180
tattcttaga	gctatagatt	tttggtcact	tgcttttata	gactatttta	atactcagca	240
ctagaggggag	ggaggggggag	ggaggaggga	gcaggcaggt	cccaaatagca	aaagccagag	300
aaaggcagat	ggggctctccg	gggctgggca	ggggtgggag	tggccantgt	tggcggttct	360
tagagcagat	gtgtcattgt	gttcatttag	agaagtgggt	gaaggttcct	gggaccttag	420
gtaaagacta	gacgcgcct	agtactggtc	tctactgtgc	tggctcagga	gttctgagaa	480
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tgcagagact	gggacagaca	ggtgcaggca	atgggccctc	ccacacccag	tcacctacaa	780
ggaattttca	aatccacttt	taaaacagaa	accggtaaat	gcgccgtatt	gtatatttta	840
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<210> 71

<211> 796

<212> DNA

<213> Homo sapiens

<400> 71

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cacttgattt	ttcccttcag	gtttctctgt	atgctgtgtt	ctctcccaag	agtggctctc	180
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tagtaaataa	tgagtataa	acttggttga	aagaccatgc	aggaaccaag	caactctttt	420
cctctgcctc	aatgcagtta	gttcaagaac	ttactaagaa	aagagtgtgt	ggccaggcac	480
agtggcacag	gcttgtaatc	ccagcactgt	gggagaccaa	ggcaggcaaa	ttgcttgagc	540
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aaagtagcca	ggcatgggtg	catgcacctg	tgggtcccagc	tactttggag	gctgaggtgg	660
gcgaatcact	ttagyccggg	gaggtcgagg	atgcagttag	ctgagattgc	gccactgaac	720
tccagcttgg	gcgacaaaat	gagaccctgt	ctcaaaaaaa	aaaaaaaaa	aaaaaaaaa	780

aaaaaaaaaa ctcgta

796

<210> 72
 <211> 532
 <212> DNA
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (434)
 <223> n equals a,t,g, or c

<220>
 <221> SITE
 <222> (528)
 <223> n equals a,t,g, or c

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gaggcgtaac tgtgcatatg gacaagggtt atattttctgt tcaaagtggc catccatag	180
cttctaggtc tcctttgtct ctggtatcaa gtgtatgtat gtatgtatgt atgtacttat	240
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gtcaagttaa taatgagctc cccaaagcca ccactgggt agcctcacat ctttttcac	360
ccctgtgcct cttccctgct tttgtcctac tctagccaga ctggtgccga agggggggcc	420
ggtamccaat tcgncctata gtgagtcgta ttacaattca ctggccgctc tttamaaagt	480
cgtgactggg gaaaacctgg ssgtacccaa cttwaatcgc cttgaagnaa at	532

<210> 73
 <211> 546
 <212> DNA
 <213> Homo sapiens

<400> 73	
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agttagtaag cagtactgat gatctgtgaa atgattctct gtggacttga gcatgctaaa	180
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agggctctat tccctcagcc tcgtccctc gaagccaca cttggaggcc aggaagttaa	480
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ctcgta	546

<210> 74
 <211> 715
 <212> DNA
 <213> Homo sapiens

<400> 74	
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taaatccca agggctgaca tgattgacat ttgccaatagc ctgaggaggg agcatttcct	180
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aggccaaagc	gggcggatca	cgagggtcagg	agtttgagac	cagcctggcc	aacatggtga	660
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<210> 75

<211> 406

<212> DNA

<213> Homo sapiens

<400> 75

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taaaagcacc	ccttcagagc	aatctcattt	ccatttcttt	caggccactt	atTTTTTcca	120
actttttttc	cgtatcttca	taaatgtttc	actcttcttt	gttagtattt	cttagtctct	180
tgagtcaaga	aatatttact	gagtatgatt	gcatgcataa	gtagtgtgcg	ttagagatac	240
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cgaagtggc	atTTTgtaag	tgTtcgaata	agcaccatgc	cgtgggataa	gaaataaaaag	360
tgtgtgcctc	atctgtaaaa	aaaaaaaaaa	aaaactcgag	ggggggg		406

<210> 76

<211> 542

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (429)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (473)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (510)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (518)

<223> n equals a,t,g, or c

<400> 76

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cttggtgttt	gatgacatta	agtatattcg	cattgttgtg	caaccatcac	tgccatccat	180
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cagtcctca	tcctccacct	cagcctctgg	aaaccactag	tctactttct	atctctgtga	300
gtttgacact	ctcagtacct	tgtacaggtg	gaaccataca	gtatttgtct	ttttgtgact	360
ggcttatgtc	acctagaata	gtatcctcga	aggggggggc	ggtaccaat	tcgccctata	420

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gtgagtcgna ttacaatcaa tgggccgctg ttttacaacg tcgtgactgg ggnaaaacct      480
ggcgggtaccc aacttaatgg cttgcaggan atcccccntt cggcagtgagg gtaataacga      540
ag                                              542

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<210> 77
 <211> 420
 <212> DNA
 <213> Homo sapiens

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<400> 77
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gattaaatta cattcagcat attcttcccg agtgcgtccc gtcttagtgg gggttagagc      180
tgcgttcagg ccagctgggg tccggttacc tctaataagg atgatgatct ggaggcttag      240
cgataattct gcactgattc tcttgtgcct gcagaacctg tggtggccaa cttggatggc      300
aggggaagat caacagaagg tgccctccac ccacgtcctc ccagcgtca ccttggtcag      360
cctggggggc aactcgtgcc gaattcgata tcaagcttat cgataccgtc gacctcgtag      420

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<210> 78
 <211> 465
 <212> DNA
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (446)
 <223> n equals a,t,g, or c

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<400> 78
gattttttcc catcgtggaa cagagtcttg ccaacttata cctctctctg agccttagtc      60
tcctcgtttg taaaatgaga gttaaaatct acctcatgga atcattgcta agattaagca      120
agatatataa gtagagcttg tgcacatggg aggtacttgg agaattgtat ttctccttcc      180
ctcttactca tctggacaag tttaactaga attctaaaca gttaaataatg tatcaatcct      240
ttgtattaaa tatcttggtg gtaaaatgtt aaaatattga tgtgaataac agctggattt      300
gaatattcaa attaggggaa ctctttcatt gttttaagat aacatctgta catttaattc      360
gtgccatgca ataaaacagc ttttcttgaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      420
tcgagggggg gscgggtacc caattngccc tatagttagt cgtat                      465

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<210> 79
 <211> 890
 <212> DNA
 <213> Homo sapiens

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<400> 79
aggttactta ttgctcctac ttcatatcat atgtggttct acaacctaca ttatcttctg      60
tatgtctttt aactagctgt gtgttcttac ataagatctg cagaccttgg ttctcaactg      120
caaaagcata ttgattaaat gattactggt tttacctgca atactttaat ttttggattt      180
gggattaata atgtaaaaaa gactaacata tatgtgggat tacaaaactg ttttgttagc      240
cttcaaacaa ctatgaactg catcaggagc tgtcttatac ttattgttct gctattaata      300
cttaatgcac tgctgtgaaa gagctgattg ctacttaaaa actctgctta aatgaaaaaac      360
caaaacataa aagattaaac caaacatact tactctccca tagccctggt ggacagcaac      420
ataaggaggg aaatgtttct gttgatcttt ggcttcaagg attaatacca gatttggata      480
ccggttagtt agataattgg taaggaatcc cataaagttg taaattacat aagcttcata      540
gcattctctg caggatccca catatattgc aattccggga tatttcaaag ctatccacta      600
tgaaaaagca cagatgttaa agatagttgc agctaagata aaatgaatca ccactccatt      660

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catggtactc	acaataagct	aatttttatg	cttgagatgt	cttgtcatat	acttacatgg	720
gactctctaa	aatttatcat	tatgagggct	atcaatctgt	gaaatgaatg	cttaaaagca	780
ataaacatct	tagatattgg	taaacaaaaa	caagtgtttg	aggggtaaat	aatgaataaa	840
gagagaagct	aaagtaaaaa	aaaaaaaaaa	aaaaaaaaact	cgtagggggg		890

<210> 80

<211> 470

<212> DNA

<213> Homo sapiens

<400> 80

ggcacgaggg	aaatcttgca	cataggcagg	taaataatta	taaatggtga	agtggattat	60
tctgagctgc	ttaattttta	agggaaagag	aacttttaac	tcttcaacct	tttatgctgc	120
taataagagt	tccacaatca	atagaaatct	atcttggcag	gcacttcctt	ttaccacta	180
gaattttttc	ccttgggagt	tcacgatccc	cagaaactgt	gatatgagcc	attcaatatt	240
gatgtactaa	aacagtgctc	tgcttaaata	cagtttttca	acatacagtc	ttggaagaaa	300
caaaatccaa	aataaattcc	aatagtccag	taacaggaat	aaagacaact	attgcaaatt	360
aaatcttaca	gacttatatg	aaagctgttg	ttaacagctg	ggtactagtt	atttgaaaag	420
tttctcgtgc	cgaattcgat	atcaagctta	tcgataccgt	cgacctcgta		470

<210> 81

<211> 1090

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (8)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (28)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (43)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (54)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (95)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (545)

<223> n equals a,t,g, or c

<220>

<221> SITE
 <222> (863)
 <223> n equals a,t,g, or c

<400> 81
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 tcgtaaccaa ctcccccca ttgaccccaa atggncggta ggcgttgtag ggggtgggagg 120
 tctatataag cagagctcgt ttagtgaacc gtcaagatcc gcctggagac gccatccacg 180
 ctgttttgac cctccataga agacaccggg accgatccag cctccggact ctagcctagg 240
 cttttgcaaa aagctattta ggtgacacta tagaaggtag gmctgcagggt accggtccgg 300
 aattcccggg tcgaccacag cgtccgccag cctggaggcc cagacgtggc gcagcgactc 360
 ggaggttcgc ctccagcttg cgcacatctt gcggccgggt cccgatgagc ctctgtttgc 420
 ctccgctggc gctgctgctg cttctcgcgg cgcttgtggs cccagccamr gccgccactg 480
 cctaccggcc ggactggaac cgtctgagcg gcctaaccgg cgcccggtga gagacctgcg 540
 ggggnatgac agctgaaccg cctaaaggag agkgaaggct ttcgtcacgc aggacattcc 600
 attctatcac aamctgggtga tgaaacacct ccctggggcc gaccctgagc tcgtgctgct 660
 gggccgcccgc tacgagggaac tagagcgcac cccactcagt gaaatgaccc gcgaagagat 720
 caatgcgcta gtgcaggagc tcggcttcta ccgcaaggcg gcgcccgacg cgcaggtgcc 780
 ccccgagtac gtgtggggcg ccgcgaagcc cccagaggaa acttcggacc acgctgacct 840
 gtaggtccgg gggcgcgcg ganctgggac ctacctgcct gagtccctgga gacagaatga 900
 agcgctcagc atcccgggaa tacttctctt gctgagagcc gatgcccgtc cccggggccag 960
 cagggatggg gttggggagg ttctcccaac cccactttct tccttcccca gctccactaa 1020
 attccctcct gccttaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1080
 aaaaaaaaaa 1090

<210> 82
 <211> 698
 <212> DNA
 <213> Homo sapiens

<400> 82
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 cccccaccct aaaacttgct gtaaagcagt tcctggaaca gagcagggtgc tcagtagtac 120
 tgggtgcatg aatgaatgaa tgaatgaata ggttttccctc ttttagacac attgggagat 180
 gggcctatgg ttctctatgc tcattttgac ccagagattt gtgtcctgtg actcacatcc 240
 agacccaaaa cacacacata cacacgcaca cataaatata cacacacaca gacacgtgca 300
 cacacagaca cacatgcaca cacacataca cacaccttg tttgaagaga agagggatgg 360
 gaacagacat tctacgcagt cctacagtgc accactgtgc ataggtaact gatgctgtat 420
 aagcactcaa ggattatctc cattttttagc cagagaaact gaggcttgct ttctgctgtg 480
 tctccagtgc ctgacactgt gcctggcata aacatctgct gaactgaatt gcactagatt 540
 caagaggctc agaaaacagt tcaagggtcac ccaactagca agttgtggag ccagaatctg 600
 tgctcagggc tgttcagtc ccagccagtg ccgggtagca gccataggca cctgcacaaa 660
 ctccagcgac ctcgtaact tccaaacacg gtctcgta 698

<210> 83
 <211> 868
 <212> DNA
 <213> Homo sapiens

<400> 83
 cagcgcgtccg cggacgcgtg ggcggacgcg tgggcaaaaa tcttaaaagc actttatcat 60
 ttcattttccc tgcactgtaa ttttttttaa tgatcaaaaa cggtatcata ccaaggctta 120
 cttatattgg aatactattt tagaaagttg tgggctgggt tgtatttata aatcttgttg 180
 gtcagatgtc tgcaatgagt aaatttagca ccattatcag gaagctttct caccaatgac 240
 aacttcattg gaagatttta atgaaagtgt agcatactct aggaaaaaaa tatgaatatt 300
 ttagcatcta tgtattgaaa attatgttga ataaatgtca gactattttt tacataacgt 360

tgctttctgtt	taattttgtc	acgttcagag	gtggggggta	ggagatgtaa	gcccttgaca	420
gcaaaataat	tccttttgct	tgatttcaga	cagttgcatc	agctcctttg	ttctgtgttc	480
atgttacact	tatttaggtg	gctgaatcca	cagaggagcc	tgctggttct	aatcggggac	540
agtatcctga	ggattcctca	agtgatgggt	taaggcaaaag	ggaagttctt	cggaaaccttt	600
cttcccctgg	atgggaaaac	atctcaaggt	gagtgttata	ataaagatct	tggcttatgc	660
aacatgaatg	ttcctcgttt	gcatcaattt	aagaataagg	tatgtttaca	cgtatataat	720
cagaactttt	aaacatacag	aattttgctt	tataaatagc	ttcgctttaa	agatctctta	780
tatatttaac	ttttcttaat	acacagcctt	ttagtacaca	caaatttaaa	aagtaggtaa	840
tgcatatatt	gaaaaaaaaa	aaaaaaaaa				868

<210> 84

<211> 629

<212> DNA

<213> Homo sapiens

<400> 84

ggcacgagaa	cctttggggc	tgacacaaga	tccttttagtg	tttgggatga	cctcttttct	60
gcagactttc	tccttatcc	ctaactcatg	catggaaaac	gtttgtcagg	ctggtttccc	120
gagcctcctg	cacctcaaca	tcacgtcac	ccttttgggt	ttagccaggt	gttatttagc	180
aaattttctc	agctgcaggg	aaggatcaga	gcactatctt	ttttttttt	tttttctcct	240
ggagccagga	ctgcacaagg	caatggccaa	atttagttga	attcagccta	ccatcctttg	300
ctgatgactc	agctctatgc	caagtactgg	agccacagag	atgggtcagt	cccagccct	360
gtcctcagga	agcccatggg	cagggaaaacg	ttgtagggat	aagtaataga	gggcagttgc	420
cttcagggtc	cctgggtggc	gctgggtccct	atgggtccct	gatgtgaatt	agaagacggg	480
gccctttcca	ggtggattca	gacctacact	agaacgcaca	gctttgggag	tgacacacag	540
gttggatttt	agcacccctt	gccccttggc	cagaggtgcc	ctgctgcacg	gccatacgt	600
gcagcctcga	gggacacaca	ggccaaagt				629

<210> 85

<211> 837

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (474)

<223> n equals a,t,g, or c

<400> 85

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atgtgcccct	ccccggtcat	atgggtccct	tctggcccct	gcccagctta	tactctgtcc	120
gactctcaca	gtcaccctgt	cccccttgc	tttctttgct	gccactgcag	gcccacctca	180
gcctctgca	cactctcttc	agatcagcct	cccaatctcc	agcgtctgga	gtgttctggg	240
gctgcctgag	agagagacat	gaatacatgt	caccctgcct	tcctcacatg	taccagaagt	300
ttgatttttt	tttttttttt	tgactgagtc	ttgctctgtc	accaagctgg	agtgcagtgg	360
cacgctcggc	tactgcaac	ctccacctcc	cgggttgacg	cgattctcct	gcctcagcct	420
cccgagttag	tggtattaca	ggcatgcacc	agcatgccc	gctaattttt	gtanttttag	480
tagagacagg	gtttcaccat	gttgccagg	atggktttga	tctcttaacc	tcgtgatccg	540
ccgccttgg	cctctcaaag	tgctggaatt	acaggcgtga	gccaccacgc	ccggccctga	600
ttattattat	tattatttta	aacaataatc	tggtccaggc	acagtggctc	acacctgtaa	660
tcccaacact	ttttgggagg	ctgaggcagg	aggattattg	agcccaggaa	tttgagacta	720
gcctgagcaa	catagtgaga	ccctgtctct	acaaaaagta	aaaaattagt	ccaggcatgg	780
tggcacatgc	ctgtagtccc	agctactcag	gaggctgaga	taggaggatc	actcgta	837

<210> 86

<211> 903

<212> DNA

<213> Homo sapiens

<400> 86

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ggcacagcct tccccctgcc cttcctgcct ggctcactcc tggccaccct tcagactcct      60
ctctctgcct cctccagctg gcgcctcact tgggtgatggc cgtgtctgtt ccatggcccc      120
tcccagaggk acttggtttc tcttgctgtc attgcgtctc ccttacgggg ccgcatgctg      180
ggtttttctta ccatttcctg catcctgcag agccgagggc gtggcagcac caatcaagtg      240
tagtaggaat gagtaggaaa caagcctcct tctccatggc acagaargga gtctgtcacc      300
ttggaaagtc aytcaagaga ggatccaaga aagcgtcttg ccctamctac ccctccttta      360
gcaagtgagg atcttcgagg graggggagt ttccaagtca actggtgaca aagccaggat      420
gagaagacac tcccagacca ctgtggctaa tgacacacac tggccggcca tgccatctgc      480
cagcgctgga ggtggccgct caacacagga aggtcaaggt catgttagca gctccccccac      540
ccagcagggg aaagggaaaag acttgccactg gggagcagtt ttattttatt ttattttatt      600
attattaatt atttttagat ggagtcttgc tctgtcacc aggtgatgc agtggtgaga      660
ttttagtcca ctgcaacctc tacctcctgg gtctcgagcga ttctcctgcc ttaccctcct      720
gagtagctgg gactataggt gtgggtgtgc atgccggtaa tcccagctac tcgggaggct      780
gagggcaggag aatcacttga acctggaagg cggaggttgt ggtgagccga gatcacacca      840
ttgcaactcca gcctggacaa caagagtga atccgtctca aaaaaaaaaa aaaaaaactc      900
gta                                          903

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<210> 87

<211> 725

<212> DNA

<213> Homo sapiens

<400> 87

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aggttctaag cattttgctt gacctgactc atttaatcct cacaaaactc tacaagataa      60
gtatatcttc actactttac aggcataaaaa tctgaggcac agaaaagtta ctgaagctcc      120
aaggtcacac tgtgtaccat aagtggaaga gctaggatgc aaaccaggc agccgggttc      180
cagagcagtg ttctaactac taccctctgt tgccctctcat tcatcccatg accttctttt      240
gtcttaccta cactgggatg tgtttgggac atgcattttg cttggtgcta tctcattctt      300
gcagaatgca ttgtacttgc tatttggtgc tattcacagt tcagggtttg ccaggcaagt      360
acaatgaagg aggagagggg caaaggaatt gaggggtgcct acaagggagt agttagagag      420
atggatgtga aatctaagct gggcaaattg agaagtaagg acatgatata ggtgatgggc      480
agtaaaaaata tgtaatgtca gcagtttaaa ggactggatg gggcagatat taattggagt      540
tgaggacta aaggagttca aaatatagga aatgaatacc agagacagag agagggctga      600
agtcaaaatg ttggaggttg tacttattat taacaacaag gtctagagga tgaccgcaga      660
attggggctc aaggtgacac atggctgaca gctgtcattg accacactgt aatgcagaac      720
tcgta                                          725

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<210> 88

<211> 606

<212> DNA

<213> Homo sapiens

<400> 88

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tgggtccccg ggctgcagat tcggccgaga attacacgaa ttaawttatt catgaggcta      60
catttcattt catatgcatg ttccagggt gtattctctt gtgcaatctg tgtatgttct      120
ttgtcttata tttttctatg ggaatatatt ctttttattc acttataaga gcaatgcatg      180
tatcaagggt agattttaat ttgcaacat attttgtggc ataatacagg ttaaaatgct      240
tgaagttacc atatatgtaa attttttctt catgttcttt gcatttaagt gactggaaga      300
gttcattcct tccactgaaa tcaactgaata actaccttgg ctacttggtg ccaatgatga      360
aggcatcata tttatacccc tcaaaggatt cacagtccag gaagaagcag acaaacgaag      420
actttcataa gtgctatgga gagccaagga accatctcga tctgtctggga attcctgggg      480

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caggaaactg aggatgggac tgtggtccaa ggaggcagac tctgaccagg ctgggacagg	540
gaaggggagc gttcaggtca aggtggtcgg ctttctgtca gagcatactg cattacagta	600
ctcgta	606

<210> 89
 <211> 1142
 <212> DNA
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (39)
 <223> n equals a,t,g, or c

<400> 89	
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gggaggacac tggggatagg ggcttggggc tattttacctg ccattttaag tagtttgcta	120
ttttagcagc caacaataac tattggtgct gaataccagc cctgcagtgt agcatgagac	180
aggtccatgc acacatgcat taggaaaaca ctttcatgaa gcaggattct gcctgggctg	240
atgcacacaa cctctatgga gggtgaaaca gtgtttctga agaccgtagt ttgggaaccc	300
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cactaccagc cagtaggtag gytggccaag agaagccagc ttgcatcacc agcatcatct	480
agggaatgga atcatggcag taatacgttg cttaggaaac aaaagctcta tggacacatc	540
ttccaccttc tcagtcccag aaaccrtatg tactgtgacc ccgctcayta ggcccagccc	600
tcgggaagag tgtgggccct tgaaaaggga agactgagtg agcaaaatga tgagaaaact	660
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tccttgatct tggagatgct gtgtgagtg cagggggact cctgctgggt aaatattcta	780
tatgtggatg cctggacagg cccctatccc aggccttgct gtgcagaagc tcccctggg	840
ccgagcgcgg tggctcacac ttgtaatctt ggcactttgg gaggccgagg caggtggatt	900
gcctgagttc aggagttcaa aaccaggctg ggcaacatgg tgaaaccctg tctctactaa	960
aaaaaaaaacta accaggcgtg gtggtgcatg cctgtaattc cagctactag ggaggctgag	1020
gcaggccaat cacttgaacc caggaggtgg aggttgagc gagctgagat cagccactg	1080
cactctagcc tgggcaacag agcgagactc tgtctcaaaa aaaaaaaaaa aaaaaaactc	1140
ga	1142

<210> 90
 <211> 596
 <212> DNA
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (4)
 <223> n equals a,t,g, or c

<220>
 <221> SITE
 <222> (8)
 <223> n equals a,t,g, or c

<220>
 <221> SITE
 <222> (28)
 <223> n equals a,t,g, or c

<220>

<221> SITE

<222> (57)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (61)

<223> n equals a,t,g, or c

<400> 90

gganaccngc	tttgeccctt	ggtttccnca	aagctcgaat	ttaccctcac	taagggnacc	60
naaagctgga	gtccccaccg	cgttggcggc	ccgctctaga	actagtggac	ccccgggct	120
gcaggaattc	ggcacgagtc	ctgacctcag	gtgatccacc	cacctcggct	tcccaaagt	180
ctaggattat	aggcttgagc	tactgtgccc	ggcccatggt	gtttttcttt	agggtctctc	240
ctacagcctt	gagaagtaga	taggcatcag	agtatggtac	tataggaatc	agaaaaattc	300
aaaacaaatg	tggattaagt	gtttaggctc	tatgtggctc	acgcagccag	aatccttaag	360
tctgtgtgtt	tctgtgtctc	aagactgggc	tcacattctg	gctttgtcca	taacaatgct	420
ctgggatttc	agggagttcc	ctcatttgta	aaatgagggg	gtcagagcag	gtgatatcca	480
tgtttcttcc	ctttctgata	ttgttgtctg	tggcatattc	tttgtatggc	gaatttaata	540
aattatatta	atgtgtctct	ttgaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	ctcgta	596

<210> 91

<211> 633

<212> DNA

<213> Homo sapiens

<400> 91

ggcagagtgt	ctctcaatgg	cttctttctt	gaagggcatac	acagccactg	tacttatcaa	60
tgctgtgtga	gccaacacag	tagtctctct	acattacaag	gatatgatta	ttcctaaact	120
tgtcgatgat	ctaggaaaag	taaaaatcac	taagtcagga	ttctcactt	ttatggacac	180
ttggagcaat	ccactggagg	aacacaatca	ccaaagtctt	gttccattgg	aaaaggcgca	240
ggtgcccttc	ttgtttattg	ttggcatgga	tgatcaaaagc	tggaagagt	aattctatgc	300
tcagatagcc	tctgaaaggc	tacaagctca	tgggaaagaa	agaccccaga	taatctgtta	360
cccagaaact	ggtcactgta	ttgaccacc	ttattttctt	ccttctagag	cttctgtgca	420
cgctgttttg	ggtgaggcaa	tattctatgg	aggtgagcca	aaggctcact	caaaggcaca	480
ggtagatgcc	tggcagcaaa	ttcaaacttt	cttccataaa	catctcaatg	gtaaaaaatc	540
tgtcaagcac	agcaaaatat	aacattgtag	ccacagacca	gataccatta	ataaaaaatc	600
tattcataaa	aaaaaaaaaa	aaaaaaactc	gta			633

<210> 92

<211> 725

<212> DNA

<213> Homo sapiens

<400> 92

ggcagagctt	ccctagcaat	aattactttg	cttaattttac	ttttttcatt	cttgtgcgtt	60
cccttatatt	tcatatatta	aatatccatc	aacattatat	aggggtcttt	aaacattatg	120
taacaagata	catattgaat	gtattacact	gcagcttgcc	ttttcatttc	agtgtgtgtt	180
ttaggtttat	ctgtgttgat	aagcgttgct	gtagtctcatt	cattttttta	acattgtata	240
gtatttcatg	atgattaaac	cacaatttat	ttattctcct	gttgatagac	aattaggatg	300
ttttcagttt	tttgctgtga	caaatactcc	cgttatgggc	attattttgt	ctccttttta	360
catagataca	aaagtttccc	tacggtatat	accaagaaat	ggaatttctg	agtttttagg	420
gtatggacat	tctcagcttt	actagatttt	gcctagtcca	tctccaaaac	tgtggactta	480
atatactttc	ccaccagcag	tatataagag	ggcctgtttc	tccacatctt	tgttaaaact	540
atatattgtc	aaatttttaa	attttgccaa	tctgggccag	acactggggc	tcacatctgt	600

aatcctgtaa	tcctagcatt	ttggaaagca	gaggcaagag	gatcgcttga	ggccaagagt	660
ttgggaccag	cctgggcaac	agagcaagac	cccgactcta	caaaaaaaaa	aaaaaaaaac	720
tcgta						725

<210> 93

<211> 601

<212> DNA

<213> Homo sapiens

<400> 93

tccccgggc	tgcaggaatt	cggcacgagg	tcggcacgac	actgccccaa	aatcaaaatg	60
gctcaagtcc	actttcaaaa	atgtcagtg	tcaccaacag	tgggtgaaaa	ggctgcctga	120
cccagcttct	cagagagcca	gtgcctcaaa	tccaatgcat	ggcaattgct	ctggggcccc	180
tgggtttaag	ctggctttgt	tatttgtggc	tgacactgga	aagcctctgc	acaaacaaga	240
tggcaagtga	tgagccggtc	agtcatact	gccttcccag	actctctgaa	ccacccttga	300
cattctgcct	ggaagcaggg	ggcttgggtg	aggtgggtga	cctcttgaag	tccccggcca	360
ggcctgtgat	tctgtaatct	ttgctttacc	ataattaggg	agggaggcag	aagagcagga	420
ggagaaacca	tttattactt	ctctgggatt	ttgacagctt	ggaaaaagag	agagacagag	480
aaacagtcca	gagaaggagc	cagccacagt	gagtttaacc	tctcagtaaa	ataaaaaatg	540
gctggacgca	cctcatcagc	tgccctctgt	caataccccg	gcccattctg	caggactcgt	600
a						601

<210> 94

<211> 692

<212> DNA

<213> Homo sapiens

<400> 94

ggcacgagct	aaaagagcta	gtttgagtaa	gctgtgtaag	acagctgctg	ctaaatagaa	60
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cttagacttc	agcatgggct	ggaccagac	cccaggatct	aacaactggc	gacgaggatg	180
gaaggaggtg	agtgggtctt	cagcccctga	gggtccccg	gacggctacg	tggccgcagc	240
atgagctgtg	gtaccgggtc	gcagtgggtg	tgcttggatg	agccccagtg	gaaacatggg	300
aggcagtgtg	cagatcccct	atgagtgtgg	agaaggcgct	gaatcacctg	gaaatgcaca	360
gcattgaaa	gaacatacct	ttgccagcag	agtcagatgg	gcatttgcca	ctatgctgag	420
ggaaatgaat	gccaatccc	tgccaggtgc	agcgcaaggga	ggaggaaact	ccgttgccag	480
cttgccccgt	agtcgcgtcag	aaaatagagc	atgaacagct	gttggggcccc	aagaggaggc	540
ccagagaccc	cccacgtgg	tggaacacat	ttcctatgg	gcctgtgtcc	ccgctgaatt	600
gagggagtta	agcaactaat	gtcgccagtt	gtgtacagac	ttagtgcagg	tcattcgagg	660
gaaggacatt	tgcgcaacct	agtcctactc	ga			692

<210> 95

<211> 1005

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (506)

<223> n equals a,t,g, or c

<400> 95

ggcacgagct	cgtgccgttg	gttttccctc	tgtctgttca	gtgggttctg	aacattcttt	60
gatggctgga	tcctactcct	ctgacatctt	agtgttgcca	agatcttgga	ccctcctcct	120
tctttctggt	ttgaggttgc	agaccgttgg	ctcatcagtc	acactggact	cacaggtggg	180

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tattatttgg cctgcagttt tcaaaatagg aaatcgtgtt aaaaaacaaa atcaaataaa 240
agaaaaacga caacaacaaa accaaaactg aacttccaat ttatcttggg gaattagcag 300
acctagtaaa atgagttctg tattctcata tggcaataat tttctggagc tgagtacctg 360
cttcttgggt cattcttaat caactcattc tttccaaaca tcttataccc agcctgtgtc 420
attcatttag gtgagctgac aaaggctagt aggaatataa atttatgacc cttagtttat 480
actctcccca gtggatctta tttaantacc cattwaaata ccatatgctt taaaaagtct 540
tctttcataa cattgagtgc acacaatatg ccctgaacta tgtaccagac actggggata 600
cgcggtgaat kacgcaagtc actctacttc caaagaactt acctctata gaggggagac 660
acacacaaca gtgataacat aaagccaaat aatatttggg ctgggagcag tsgctcatgc 720
ctgtaatccc agcacttcga gaggtctgag cgagcggatc acgaggtcaa gagattgaga 780
ccaacctggc caacatgggt aaatcctgtc tctactaaaa atacaaaaat tagctgggtg 840
tgggtggcagg tgcctgtaat ccagctact tgggaggtcg aggagggaga attgcttgaa 900
cctgggaggg gaaggttgca ttgagccgag attgtgccac tgcactccag cctggtgaca 960
gagcgagact ccatctcaaa aaaaaaaaaa aaaaaaaac tcgta 1005

```

<210> 96

<211> 612

<212> DNA

<213> Homo sapiens

<400> 96

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gggatctgtg taagacaaaa ttaatagctg tatctggagt actctaaatg tggatttata 60
cactaaccta tatattgac aattcctcta tgcttgcttt ggttttgagc aaattatatt 120
taaaataagtt tgttgctagg aatgtcttaa aaagctactc accctttttg ttagaagtaa 180
gtaaatgatt atgtcaggac ctgccattaa cttggtatag tacgaatata tcctcagaat 240
actgataaaa tggtatgtct tgaaacaaat cacaaactgt caatatgttg gtgatgaatt 300
tcttctgttt tcatttggat cagtagtggg gcagttcacc aagtgtgaga tcgacattta 360
atgttttcat gaaatgcaaa cccatcagtg gctaatttgt taaaaaatag atgttgggct 420
tttcttaagg ctaaattgtt cccatttgtt ttagagaaca actcacttag cctatgagtt 480
tatgcaattt ggcagaaagt gaaaacatat ttggaagtat tgaaagtcac tcattgttga 540
tcttttatat tggaatgycc aaggttgcac catcagagtg tcgttatgaa aaaaaaaaaa 600
aaaaaactcg ta 612

```

<210> 97

<211> 670

<212> DNA

<213> Homo sapiens

<400> 97

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gctcgtgccc aactcgtgcc gacgaaaagc tgccaagttg aaaatggacg agtaatcgcc 60
tgctttgatt cattgaaaaa ctaaatctcc ataccactt catccgtgtt tttggcttat 120
gtatgggatg ctagaatggc ctatctccat gtattttgtt gcatttctcc attgcttctt 180
gtgttctggc gggaatcttg gtgattcttt tcaagcacta cctgagctct gtgccaattg 240
ttcctcttct ccaggggtgt tgtgctgcgt ggtcatgtct ccacttcctt agccctgtcc 300
attgacagaa ccttggttgc tgtgatggct gcctctaaac ccttgtgaaa gcggggaata 360
ttcctcccc tgctgtaca gttgagcacc gtgtgggta ccatgttgcc ctctacactt 420
gctttcagtt gtttaaggctt cccaagcttt ggctgtggct cagtgtacct gctgtcaaaa 480
ccctgaaact ttcctagcct ggacactcag tggtagcagc aggtgttggg atttctccaa 540
gcccctaaga ctctgggagg aagagaatgg ctgtttgaca tagacctcag gagttttcaa 600
agcaccaaga aacctctcca gaagatatgt aaagatttta aagggaaaaa aaaaaaaaaa 660
aaaaactcga 670

```

<210> 98

<211> 619

<212> DNA

<213> Homo sapiens

<400> 98

gcggcacgag	tgatatttca	cgtcacatgg	ctagtgaagt	ggtaggcctc	tcttcactta	60
ttacacttct	gcttctaagc	tgtgttcttt	cctgtattac	actggaggaa	ggagaaaaag	120
aacttgtatt	tggtccttga	ctgggtggaa	tatcctttaa	tgtggctgta	aggacatggg	180
tagaatactc	tggtcaattc	atttcttatt	taaatagtga	caaagggtatg	tccatgttaa	240
ccattttctc	cttatgcttt	atacataagg	atggcttata	gggaatgttg	ctttattata	300
tcacttaaaa	tgtttggtca	ggcaatagtg	actcatgcct	ttaatcccag	tacttttgaa	360
ggacaagtca	ggaggatcgc	ttgagaccag	gaactcagga	ccagcctgga	cgacaaaaca	420
ggatctcgtc	tctacaaaaa	ataaaatagt	cgagtgtggt	gatgcagtat	tgtagtccca	480
gctatttggg	aggctgaggt	gggagtatcg	cttkagacca	ggagttcaag	gatatagtga	540
atgatgatcg	ctccactgca	ttccagcctg	gacaacaaag	caaaacccta	tttctaaaaa	600
aaaaaaaaaa	aaactcgt					619

<210> 99

<211> 703

<212> DNA

<213> Homo sapiens

<400> 99

gcttggttac	gtttatagct	tcaacacgcc	tctcattkta	ggtttataca	tgtgtttgct	60
tgtcatttta	ttttgtcatc	atttgtcat	tttattacca	gttattgagw	gcctactgtg	120
taccaggcac	tgggcaagg	gcattctgtg	agagagggt	tggtacctgc	gggcttaagt	180
agtcctgtgg	cttgtgagga	aaacgctaga	ttagatcttg	attactgtaa	atgtcaarta	240
tggtcaagt	tggtatttcg	tggtcaggag	gagctttcct	ggaatttgc	tttcttgct	300
caatttgcct	gatagtcatt	tcatgctagg	gatgttttaa	agtctctggg	gaggccctgc	360
agtgtagagg	aaaatgctga	tccacaccag	aaatgcgaac	ctggctctct	gcccttgggc	420
aagtcactta	accctcctga	gcctcagttt	ccatctgtca	cttagagctg	attataccta	480
cttaacaccc	aggctttttg	tgaggggcat	tatctcatta	gagataatgt	ttttaaagc	540
tctttgtaaa	ttgtgtagca	ttcaaatgga	agttattgtt	atttttatta	ttgagtgcct	600
tctaattcaa	cactgggata	gtaacaaaag	aagagagggg	ttattatcac	ccctcttccc	660
tgtcacgttt	agattggggc	aaggaaaggt	tctcacctcg	cga		703

<210> 100

<211> 762

<212> DNA

<213> Homo sapiens

<400> 100

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tgacgtgcaa	aggetatttc	ttgaatttta	ttaaaatgca	aaaagatgca	tccatgtctt	120
ctctaaaagg	actgcgtatt	cctccacact	tggggaaatg	cagcttgtgc	tatttcacag	180
gctcatcatg	cccctttttt	ttgccaggac	gctggttgat	taatgccatg	cttggggagt	240
gctccagcca	gaaatgaggg	ctatcgccctg	tggtcaataa	cagagcagat	tctcaataaa	300
catccccctg	gtgttacact	taatggggct	tgtttttcca	aactgctccc	tttcctgggc	360
tctgagcagc	tgagccgaga	gctcgtaagc	tctgctgccc	cagaacattg	tgcatctcyt	420
gattttgaaa	artctttcct	gaagsctcct	cttgggtcat	tggtacagcc	caagagcaaa	480
ggatttaaaa	gggccaattt	gatagggaca	gctcatagcc	ctgtgtaaga	ccactgggca	540
tttttcctgt	ttggggaaat	ggttactgga	ttagcatttt	gctgtacagg	gcggctcgca	600
agaatgtgtg	ctcttgcttg	tcttcaaagc	aggcttgtga	ggagctttct	gttcccagcc	660
ctgccatttc	ctcccaattg	gctggggccag	atgctccaga	cacagttaat	gagatgctga	720
gtgaaacaga	gccgctggct	cacatggcct	cagcctcctc	ga		762

<210> 101

<211> 650
 <212> DNA
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (497)
 <223> n equals a,t,g, or c

<400> 101
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 gagaaggcag gtgggagggc gtgacagcgg cgaggatgag gaaggcagcc aggcctgcag 120
 gcagccctga gagcatgaag cagaggggtg agcagggtcc cctcctcctg ccacccttgc 180
 tcctctctac caggctcttg ccttgctggg gtgtacccac agaactctga ggctctggcc 240
 tagccagaaa gagtgtgggt gcttctcagg gtcataatta ccccatgccc cacaggggtg 300
 gagtcactgg tagcagagtc ctccccaatc ccccccagaa gagtgtgggt aaaggcccgg 360
 gccactgggg tgtcgagagt gccaggcctg acctactggg ggtgggtgtca gtaggggcca 420
 tataccctgt tctcamgaca accccaggcc aactcagatt tgtggagcgg ccatccacc 480
 tccttccggc tcttcancct cacaggagcc tgggtgggtcg ggaaaactga ggcttagaga 540
 ggcaaaatga tgatacaatg aagagtgagt acatgtggaa caccctctgt gcctcacact 600
 ccactaagct cctcacacca ttcacttact caggcctcac cggccctcga 650

<210> 102
 <211> 360
 <212> DNA
 <213> Homo sapiens

<400> 102
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 aaggccctat gaaaacctga aaccgaggca aggtgacaaa gtctggtcat tcagcactaa 180
 gggccgcctc agattacttc tttacttaga aaaacaaaat gttgttgcaa aagattcaga 240
 gtcacaaaata ttcttcccg gctgtcagtt ttctgaattc ttagatcttt catttaattt 300
 agccatcagg gaattttctga gactagaaat acctaggcag aacccaaaaca aaatctctga 360

<210> 103
 <211> 817
 <212> DNA
 <213> Homo sapiens

<400> 103
 ggcacgagct caggttgagg ccggagagaa aggcctgggg accacctgac tctggggccac 60
 ccgggcctcc tcaggtcttc ggccagcgt gtccctgcca cggtagttgg ggttccaatg 120
 gctgaggctt ctccctgtct gtggcttgg catgccattg gccgcgtctc tatttcctca 180
 tctgagactc gggtgaccac agttctcagt tcaccgtgtt cggtagaggt gacatgaagt 240
 gcttgaccac catgtgggtt tccctgtggg attctgacct gcttcggagc tgccctctgc 300
 tctcatccc acacttctct gtgtttctca tcctggcggc tgtgtcctgt ctgccctct 360
 caactgcaac acgctggaga ggtcgggacc ctgtcttgct cattatctgt ctactaaaga 420
 acctgcaaaa tggaaaaata acaatatgtg ctgaattaat tattagctta aaatttaaaa 480
 cttaagtagc atgatttgag tgcagccagc atcacctgcc gtgagatcgg tgctgtctac 540
 aggaggatgg agcttttgg gaaccactga gctgggagta gctacgggca cctttacca 600
 gtcccaaat gtggaacatt tgagtttaaa aagcagaaaa ctctacagtt aaaagccaat 660
 attaaggttg agtccattaa tctaaattaa tctgattttt tatttcttta aataaaaaag 720
 taatcctatg caatcaaagt taaagttcgt atatggctcc ctatgaggta ctacattccc 780
 tgaagtgtca caaaaaaaaa aaaaaaaaaa aaaaaaa 817

<210> 104
<211> 881
<212> DNA
<213> Homo sapiens

<400> 104
ggcagagta tgactaataa ggtaaatctgt ccttggttaac aagcctgtat ttgttatacc 60
tgtacttaaa gtaaaattca aactccttac cctgtcctac aaggctctac ctgatctggg 120
ccctacctca tctctaacat catcttatgc tattttcttt cttgttcacc agagccacac 180
cagctacctt tctgtccctc cttgttagac ttattttctgc tttagagcac ccttgctgct 240
gccaccacct gaaatgcttc tcttctggta ttttattttg gtgagaacac ctggcatgag 300
atctaccctc taacagattt ttaagtgtat aatacagtat tgctgtctgt aggcacaatg 360
ctgcacagca gatctctaga acttaccttg tataactgaa attttatact cattgattag 420
caacagcccc aaattattga aacctccttg aagcctaaat ttcagaaatg ttcaaatggt 480
tgaaaatgg atattctgaa ttatcttatt agcatctacc tataatttagc actgaaaata 540
gtaatttttt taataaagaa tcagtttaagg gccgggtgtg gtcctcacgc ctgtaatccc 600
agcacttttg gaggctgagg cgaggagatc acaaggctcg gagatcgaga ccatcctggc 660
taacaccgtg aaaccctgtc tctactaaaa aaatacaaaa aaaatcagct gggcgtggtg 720
gcaggtgcc aatagtcctc ctacttggga ggctgaggtc aggagaatgg cgtgaaccca 780
ggaggggttg agtgagccaa gttctcgcca ctgcactcca gcctgggcga cagagcgaga 840
ctctgtctca aaaaaaaaaa aaaaaaaaaa aaaactcgta g 881

<210> 105
<211> 655
<212> DNA
<213> Homo sapiens

<400> 105
ggcagagctg gtctcgaact cctgacctca ggtgatctgc ccaccttggc ctcccaaagt 60
gctgggatta caggcataag ccattgcgct cggtgagat tagcaataat taatgtgata 120
tgaaaatatt ttctttttct tcatgacaaa ttcatggcta atactgccag gatttttttg 180
ttgttgcccc tattcataat agaaggaaat gctaatatga aaataaagat gtcacttttt 240
ccccaatcca tgcaatttcc ccctaaattg tatccatgac ctacctgagg gggatccatg 300
gactctcagg ttaagacccc tctactgaag ggtagcagag tacagtttca aaattactga 360
ttaagagcgt gggctcacca ggagttcaag ccagccggg gcaacaggat gagacctcat 420
ctttacaaaa aatgaacaaa attaggcatg gtggtgcttg tctgcagtcc cagctacttg 480
ggagactgag ttgagaggat cacttgaggc tgagaggttg aggggtgcagt tgagctgaga 540
ttgcaccact gcactccagc ctgagtgaca gagtgagatc ctgactcaaa aaaaaaaaaa 600
aaaaaaaaaga aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaac tcgta 655

<210> 106
<211> 606
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (9)
<223> n equals a,t,g, or c

<220>
<221> SITE
<222> (19)
<223> n equals a,t,g, or c

<400> 106
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 taatggaaac tcaaatttgc ctaactcaga ttgttagcact tttcttcttc aggctagtc 120
 taggaaaact cacttgtttt ttgtatggaa aactagtgtt agtagaagcc tttattcttg 180
 catagccccc aaatcagctt tttcagctat aatttagtaa gtctaattgtg ttcgactgaa 240
 gtactttttt ttgttaataa caagtgaata ataatgaaga gtgtgtcctg gcgcatggct 300
 cagcctgtga atcccagcac ttcgggaggc cggagcygag gcagcggatc acttgagggt 360
 caggagtcca agaccagctt gaccaacatg gtgaagtcct gtctctatta aaaatacaaa 420
 aattagccag gtgtggtagt gcatgtctgt aatcccagct acttgggagg ctgagacagg 480
 agaattgctt ggacctggga ggcggagggt gcagtggagt gagattgcgg cattgcactc 540
 cagcctggac aacaagagtg aaactttgtc tcaaaaaaaa gaaagaaaaa aaaaaaaaaa 600
 actcga 606

<210> 107
 <211> 657
 <212> DNA
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (634)
 <223> n equals a,t,g, or c

<220>
 <221> SITE
 <222> (650)
 <223> n equals a,t,g, or c

<220>
 <221> SITE
 <222> (655)
 <223> n equals a,t,g, or c

<400> 107
 gagtttgtra acctatatcc acagcattaa ctaatcatga ttcgccccat atttcactgg 60
 ttatgctttg gttatcctag aaaagaaccc agggcattta tgaggtaaaa cttgcagggc 120
 agattacagg catgagccac cgcgcctaga cttattagtc ttttttaatg ggatgacagc 180
 agctgggrtg tatatatcc tgcaggaaag aaaaggaaat ggcttcacat tgctggatgg 240
 gagcagtatg tgtgttgtt ctgggtataa tcttcttagc tgcacttttc ccatacatt 300
 ctttctacta aaaatcatga aagtttgaat tatagttcct ctcacaggat tgaaagcaag 360
 tatcagagga gtcattccatt caaaacacag ttcttccact gcagtatccg atatgttttg 420
 tatgtgcgct aggtgtgctt ttcattcagt ctacaataca gttcaccagt gtggagacct 480
 tttgccctgc ctgatttggt ttgttttggt ttactcactc ttttcaatga cttttgggtt 540
 tggccagtat gaagagtaat ggatgttgga atacctcttg ccagttaaaa aaaaaaaaaa 600
 aaaaaaaagg gcggccgctc tagaaggatc caanttaagt aagcgtgtcn ctcncnt 657

<210> 108
 <211> 605
 <212> DNA
 <213> Homo sapiens

<400> 108
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 ggcattggatt tgggcatttg tccagggttat gaagcacatc caccagggtg gcctgggtgga 120
 gttaaaggcc atccctactg ggcaggatgt gctggtgcca gttgggtgag ttcagaggtg 180
 gttgggagag agaaatgctc agagctctct gtctgtctac ctgtccctga ctctcagtc 240

cagcaccac	ccaccccatg	gtccccactc	atccgggagc	ttacagcagc	ccctccacct	300
ctatccagcc	atcttctcta	gccataacat	tggtagctgg	caaagtgtcc	cagcacaagg	360
cctggcacac	agttgggtgt	tagtgtttgc	taaatgaatg	aatggattaa	taagaacgaa	420
tattgtgcag	aaaaagtaaa	ttcttctgga	cacttccagc	ctatatgtgg	aggggacaaa	480
gttttttgtt	gttgttgttg	ttgttgttgt	tgtgtttttt	gagacagtgt	cgttctgttg	540
cccaggctgg	agtgcagtgg	tgcatcaca	gtcactgca	gccttgatct	cctcagcctc	600
tcgta						605

<210> 109

<211> 504

<212> DNA

<213> Homo sapiens

<400> 109

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accacccac	tccctgcca	ggtgcagttt	tggtagtgcc	tgtgttgctg	ctacatccat	120
ggctcctggt	ggggaccct	ctcccaaagc	tccagtcct	gcaatgcttc	agtaactgca	180
ctcagctcag	gctgtttag	acctagggcc	agcagtccta	cagtgcctca	ccatcgcttg	240
ttccctatgc	ctgcccacac	atctgtaaat	agtccttca	tttcacatcc	ttcagttaga	300
ccctttgagt	atgccatctg	cttcgggtca	ggacaatgat	tgattctatc	tgaatcaaac	360
ctgtccttta	tttgaacagg	acatcaagtc	tagaaaaaca	agttaacacc	ttgagataac	420
aaacaaatcc	agaatttggg	accattttact	agtctggttc	tttcaaaggt	caatgttata	480
aaaaaaaaa	aaaaaaactc	gtag				504

<210> 110

<211> 770

<212> DNA

<213> Homo sapiens

<400> 110

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tggattttcta	tgccacacta	cccgttaact	tgaaaaataa	ctttaggctg	cagttttcag	180
caaacaggac	agtccttagc	tgccacatag	ctcaacataa	agtgcacaaa	aaacttcacg	240
gtgggacagt	gaatcataaa	ttcccaaact	gacgtgtgtc	tacagaacag	atgagaactg	300
ttactcagtg	tgtatcttag	gagcttttct	gcagtttccct	cacactccgt	cacattttaa	360
atgtggacac	ttgtttatct	cattagggag	gaggcgaggg	actaatgtcc	accctgcccc	420
gagtatttctg	aatatcctta	gtgaagagga	ggaaagcaag	aattctgttc	taaaggccac	480
caggctaagc	actagaatcg	cattctcttc	ctgtttgtat	gtttatgtca	gcagttgcca	540
cagatgtgtt	aatattgttt	tcctggtaga	gaattaaggt	gttcgttcat	ctcaaaacaa	600
atcccgtaac	ctgcacacaa	aactccagct	tcctaattgca	aagagaagag	aatattgatt	660
ataagctgct	tgatattctt	tttatcccca	gccccctcaa	ataccagcct	ggaagtctgg	720
acattactaa	aatttaccag	tctcaaaaaa	aaaaaaaaaa	aaaactcgag		770

<210> 111

<211> 751

<212> DNA

<213> Homo sapiens

<400> 111

ccacgcgtcc	gaggacgcgt	gggagtcac	tgtcttaagt	tggaaaaaag	tttcatatga	60
ttctttccca	tttcccctgt	attccttttc	attataccct	cattccttga	acagaattgt	120
tattgttttg	tttttccatc	cacaccccta	taatgcaacc	ttcctgtgta	aatttttaggc	180
ttaagctttt	ctattcacat	acttttatgc	tgaggcttgg	atttttattt	gggctgttag	240
atgcccatct	tgacattgac	attaggggtt	tcaaacacac	cttaaaaggt	tagatgtgac	300


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ttgcaatggt attgaacaat ttgatgatcc gggatattat ggctctatga aatctccatg      360
gttcttggag ctagcttggt tttattctgg gaagaatttt ctagctcccc agcttacggc      420
ctgaatgggt agagtccagc cagtgcgtgt tgactttata gttcaaaggg ggtcatttct      480
gtggtcacta tcctatttaa cagtcattgt atggtaggtc aaggtaggtc atcatataaa      540
taatctgcat tctgttttga ctgttttatt tttaaaaata atatctcttc cttttaaaact      600
ttaaaaaatt tagtaaagtt tagtaaacct tcaaaaaatt agtaaaaaat gtagtaaaaa      660
ttcacttcct tcattatgct ttttgaaatc tggctttttt tctcattctt cccctattaa      720
tggttcttaa aaaaaaaaaa aaagggcggc c                                     751

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<210> 112

<211> 543

<212> DNA

<213> Homo sapiens

<220>

<221> SITE

<222> (22)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (42)

<223> n equals a,t,g, or c

<220>

<221> SITE

<222> (51)

<223> n equals a,t,g, or c

<400> 112

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cgctgcccgc ttggaggggc gncactagtg gatccaaagg antcggcacg ngctaccctt      60
tgccmaagcc taaacttcat actagatata caactgccta ctggacatct ccatttataa      120
gcctagtagc ctaataagca taacctcaga cttaccaggc ctccactga agtcatgaac      180
ttcagcccaa cccccatgcc agggcaaaac ctgtgtgtta cctcttattc ctctcttgcc      240
tcatcccatc catgttcagt ctgtcagtg atcctgtgag tccagtcttg aggatagttc      300
caggatctga tcaacttctca ctgcctcttt tgctgccacc acctctggcc tggataattg      360
cagcagcctc ccagttagcc ttgctgtgtc catccttggt ttccccctct gtctgtcttc      420
aacagaggag ctagtgattc tcttaggaca gaataaatca tttaggtttt cttcacatgg      480
tcctgaagaa gcttcctacc tcaactcagt taaaaaccaa aaaaaaaaaa aaaaaaaact      540
cga

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<210> 113

<211> 86

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (2)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 113

```

Met Xaa Leu Gln Pro Asn Pro His Ala Arg Ala Lys Pro Cys Cys Tyr
  1              5              10              15

```

```

Leu Leu Phe Leu Ser Cys Leu Ile Pro Ser Met Phe Ser Leu Ser Val

```

20 25 30
 Asp Pro Val Ser Pro Val Leu Arg Ile Val Pro Gly Ser Asp His Phe
 35 40 45
 Ser Leu Pro Leu Leu Leu Pro Pro Pro Leu Ala Trp Ile Ile Ala Ala
 50 55 60
 Ala Ser Gln Leu Ala Leu Leu Cys Pro Ser Leu Phe Ser Pro Ser Val
 65 70 75 80
 Cys Ser Gln Gln Arg Ser
 85

<210> 114
 <211> 20
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (20)
 <223> Xaa equals stop translation

<400> 114
 Met Ala Ala His Ser Val Leu Ser Phe Leu Leu Trp Thr Pro Tyr Ala
 1 5 10 15
 Leu Lys Ser Xaa
 20

<210> 115
 <211> 39
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (39)
 <223> Xaa equals stop translation

<400> 115
 Met Leu Lys Leu Ala Thr Ile Leu Leu Thr Leu Leu Leu Lys Asn Leu
 1 5 10 15
 Asp Ala Gly Leu Thr Asp Lys Leu Ser Arg Ser Asn Phe Ile Thr Asp
 20 25 30
 Phe Ile Leu Thr Lys Tyr Xaa
 35

<210> 116
 <211> 88
 <212> PRT
 <213> Homo sapiens

<220>

<221> SITE

<222> (86)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (88)

<223> Xaa equals stop translation

<400> 116

Met	Leu	Leu	Leu	Tyr	Leu	Gly	Ile	Glu	Val	Ile	Arg	Leu	Phe	Phe	Gly
1				5					10					15	

Thr	Lys	Gly	Asn	Leu	Cys	Gln	Arg	Lys	Met	Pro	Leu	Ser	Ile	Ser	Val
			20					25					30		

Ala	Leu	Thr	Phe	Pro	Ser	Ala	Met	Met	Ala	Ser	Tyr	Tyr	Leu	Leu	Leu
		35					40					45			

Gln	Thr	Tyr	Val	Leu	Arg	Leu	Glu	Ala	Ile	Met	Asn	Gly	Ile	Leu	Leu
	50					55					60				

Phe	Phe	Cys	Gly	Ser	Glu	Leu	Leu	Leu	Glu	Val	Leu	Thr	Leu	Ala	Ala
65				70					75						80

Phe	Ser	Ser	Met	Asp	Xaa	Ile	Xaa
					85		

<210> 117

<211> 39

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (39)

<223> Xaa equals stop translation

<400> 117

Met	Tyr	Lys	Phe	Leu	Tyr	Leu	Val	Leu	Glu	Asp	Phe	Val	Ala	Phe	Ile
1				5					10					15	

Arg	Gly	Ser	Phe	Pro	Pro	Gln	His	Thr	Arg	Ser	Leu	Val	Phe	Trp	His
			20					25					30		

Val	Cys	Gln	Leu	Glu	Tyr	Xaa
			35			

<210> 118

<211> 27

<212> PRT

<213> Homo sapiens

<220>

<221> SITE
 <222> (27)
 <223> Xaa equals stop translation

<400> 118
 Met Met Met Met Ile Gln Thr Leu Met Val Met Ala Lys Ile Leu Cys
 1 5 10 15
 Leu Lys Gln Pro Leu Ser Met Ala Gly Ser Xaa
 20 25

<210> 119
 <211> 22
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (13)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (22)
 <223> Xaa equals stop translation

<400> 119
 Met Lys Glu Asn Pro Leu Leu Leu Leu Ile Cys Ile Xaa Gly His Leu
 1 5 10 15
 Val Val Pro Pro Asn Xaa
 20

<210> 120
 <211> 96
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (96)
 <223> Xaa equals stop translation

<400> 120
 Met Tyr Arg Asp Ser His Ser Val Leu Ala Leu Asn Trp Lys Val Val
 1 5 10 15
 Ala Thr Leu Lys Tyr Phe Leu Leu Tyr Val Ile Ile Leu Tyr Asn Leu
 20 25 30
 Glu Arg Asp Asn Gly His Ser Asn Tyr Glu Asn Tyr Glu Leu Gly Asp
 35 40 45
 Lys Ser Leu Asn Leu Leu Phe Tyr Asn Ser Met Tyr Lys Leu Val
 50 55 60

Phe Pro Tyr Ile Phe Thr Phe Ser Ser Phe Leu Ile Ser Ser Tyr Thr
65 70 75 80

Ser Ile Leu Tyr Lys Met Phe Tyr Ile Gln Arg Thr Val Lys Ser Xaa
85 90 95

<210> 121
<211> 36
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (36)
<223> Xaa equals stop translation

<400> 121
Met Lys Glu Arg Thr Arg Ile Pro Cys Ala Phe Pro Phe Leu Leu Phe
1 5 10 15

Gln Thr Arg Val Gln Thr Ser Pro Ala Phe Gln Pro His Pro Leu Tyr
20 25 30

Phe Thr Ala Xaa
35

<210> 122
<211> 38
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (38)
<223> Xaa equals stop translation

<400> 122
Met Thr Ser Val Ile Val Leu Phe Ile Leu Lys Val Phe Phe Lys Tyr
1 5 10 15

Phe Ser Thr Thr Ser Phe Leu Asn Ala Cys Ile His Phe Ile His Lys
20 25 30

Cys Lys Leu Val Asn Xaa
35

<210> 123
<211> 342
<212> PRT
<213> Homo sapiens

<220>

<221> SITE

<222> (342)

<223> Xaa equals stop translation

<400> 123

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Met Leu Gln Pro Thr His Leu Ser Leu Gln Leu Arg Leu Gln Cys Leu
 1             5             10             15

Ala Ala Ser His Leu Val Thr Leu Leu Ile Cys Leu Met Ala Pro Ala
      20             25             30

Ser Ala Thr Gly Gly Ser Ala Asp Leu Phe Gly Gly Phe Ala Asp Phe
      35             40             45

Gly Ser Ala Ala Ala Ser Gly Ser Phe Pro Ser Gln Val Thr Ala Thr
      50             55             60

Ser Gly Asn Gly Asp Phe Gly Asp Trp Ser Ala Phe Asn Gln Ala Pro
      65             70             75             80

Ser Gly Pro Val Ala Ser Ser Gly Glu Phe Phe Gly Ser Ala Ser Gln
      85             90             95

Pro Ala Val Glu Leu Val Ser Gly Ser Gln Ser Ala Leu Gly Pro Pro
      100            105            110

Pro Ala Ala Ser Asn Ser Ser Asp Leu Phe Asp Leu Met Gly Ser Ser
      115            120            125

Gln Ala Thr Met Thr Ser Ser Gln Ser Met Asn Phe Ser Met Met Ser
      130            135            140

Thr Asn Thr Val Gly Leu Gly Leu Pro Met Ser Arg Ser Gln Pro Leu
      145            150            155            160

Gln Asn Val Ser Thr Val Leu Gln Lys Pro Asn Pro Leu Tyr Asn Gln
      165            170            175

Asn Thr Asp Met Val Gln Lys Ser Val Ser Lys Thr Leu Pro Ser Thr
      180            185            190

Trp Ser Asp Pro Ser Val Asn Ile Ser Leu Asp Asn Leu Leu Pro Gly
      195            200            205

Met Gln Pro Ser Lys Pro Gln Gln Pro Ser Leu Asn Thr Met Ile Gln
      210            215            220

Gln Gln Asn Met Gln Gln Pro Met Asn Val Met Thr Gln Ser Phe Gly
      225            230            235            240

Ala Val Asn Leu Ser Ser Pro Ser Asn Met Leu Pro Val Arg Pro Gln
      245            250            255

Thr Asn Ala Leu Ile Gly Gly Pro Met Pro Met Ser Met Pro Asn Val
      260            265            270

Met Thr Gly Thr Met Gly Met Ala Pro Leu Gly Asn Thr Pro Met Met
      275            280            285

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Asn Gln Ser Met Met Gly Met Asn Met Asn Ile Gly Met Ser Ala Ala
 290 295 300

Gly Met Gly Leu Thr Gly Thr Met Gly Met Gly Met Pro Asn Ile Ala
 305 310 315 320

Met Thr Ser Gly Thr Val Gln Pro Lys Gln Asp Ala Phe Ala Asn Phe
 325 330 335

Ala Asn Phe Ser Lys Xaa
 340

<210> 124

<211> 219

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (139)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (217)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (219)

<223> Xaa equals stop translation

<400> 124

Met Val Ser Trp Met Ile Cys Arg Leu Val Val Leu Val Phe Gly Met
 1 5 10 15

Leu Cys Pro Ala Tyr Ala Ser Tyr Lys Ala Val Lys Thr Lys Asn Ile
 20 25 30

Arg Glu Tyr Val Arg Trp Met Met Tyr Trp Ile Val Phe Ala Leu Phe
 35 40 45

Met Ala Ala Glu Ile Val Thr Asp Ile Phe Ile Ser Trp Phe Pro Phe
 50 55 60

Tyr Tyr Glu Ile Lys Met Ala Phe Val Leu Trp Leu Leu Ser Pro Tyr
 65 70 75 80

Thr Lys Gly Ala Ser Cys Phe Thr Ala Ser Leu Ser Thr Arg Pro Cys
 85 90 95

Pro Ala Met Arg Arg Arg Ser Thr Arg Thr Ser Cys Arg Pro Arg Ser
 100 105 110

Ala Ala Thr Arg Pro Cys Ser Ala Ser Gly Ser Gly Ala Ser Thr Leu
 115 120 125

Pro Pro Pro Leu Leu Cys Arg Leu Pro Pro Xaa Val Arg Gly Arg Trp
 130 135 140
 Pro Ala Gly Cys Gly Ala Ser Pro Cys Arg Thr Cys Ala Pro Ser Leu
 145 150 155 160
 Thr His Leu Pro Leu Pro Thr Met Thr Pro Ser Thr Trp Arg Thr Arg
 165 170 175
 Cys Pro Thr Gly Gly His Pro Leu Gly Thr Gly Pro Gly Ala Cys Arg
 180 185 190
 Thr Ala Thr Pro Arg Met Ser Val Gly Gln Ile Leu Arg Gln Ser Pro
 195 200 205
 Gly Arg Gln Pro Gly Pro Glu Arg Xaa Pro Xaa
 210 215

<210> 125
 <211> 266
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (15)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (96)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (98)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (119)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (161)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (170)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (189)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (197)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (200)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (230)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (235)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (244)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (245)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (247)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (266)

<223> Xaa equals stop translation

<400> 125

Met	Ser	Met	Ala	Val	Glu	Thr	Phe	Gly	Phe	Phe	Met	Ala	Thr	Xaa	Gly
1				5					10					15	

Leu	Leu	Met	Leu	Gly	Val	Thr	Leu	Pro	Asn	Ser	Tyr	Trp	Arg	Val	Ser
			20					25					30		

Thr	Val	His	Gly	Asn	Val	Ile	Thr	Thr	Asn	Thr	Ile	Phe	Glu	Asn	Leu
		35					40					45			

Trp	Phe	Ser	Cys	Ala	Thr	Asp	Ser	Leu	Gly	Val	Tyr	Asn	Cys	Trp	Glu
	50					55					60				

Phe	Pro	Ser	Met	Leu	Ala	Leu	Ser	Gly	Tyr	Ile	Gln	Ala	Cys	Arg	Ala
65					70					75					80

Arg Pro Leu Ala Gly Phe Xaa
35 .

<210> 127
 <211> 93
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (93)
 <223> Xaa equals stop translation

<400> 127
 Met Leu Leu Tyr Leu Tyr Ser Leu Gly Ile Ser Val Leu Ile Ile Ser
 1 5 10 15
 Phe Pro Thr Asn Ser Ser Ile His Val Arg Lys Asn Met Ala Asn Gln
 20 25 30
 Tyr Leu Lys Gly Ala Ile Phe Gln Ser Ser Gly Phe Gln Ser Val Ala
 35 40 45
 Gly Gln His Trp Gln His Leu Asn Leu Leu Gly Thr Leu Leu Lys Met
 50 55 60
 Gln Ile Leu Ser Pro Thr Leu Val Leu Leu Asn Trp Glu Thr Gly Val
 65 70 75 80
 Gly Pro Ser Ser Leu Cys Phe Asn Met Phe Ser Lys Xaa
 85 90

<210> 128
 <211> 196
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (196)
 <223> Xaa equals stop translation

<400> 128
 Met Glu Leu Ser Glu Ser Val Gln Lys Gly Phe Gln Met Leu Ala Asp
 1 5 10 15
 Pro Arg Ser Phe Asp Ser Asn Ala Phe Thr Leu Leu Leu Arg Ala Ala
 20 25 30
 Phe Gln Ser Leu Leu Asp Ala Gln Ala Asp Glu Ala Val Leu Asp His
 35 40 45
 Pro Asp Leu Lys His Ile Asp Pro Val Val Leu Lys His Cys His Ala
 50 55 60
 Ala Ala Ala Thr Tyr Ile Leu Glu Ala Gly Lys His Arg Ala Asp Lys
 65 70 75 80
 Ser Thr Leu Ser Thr Tyr Leu Glu Asp Cys Lys Phe Asp Arg Glu Arg
 85 90 95

Ile Glu Leu Phe Cys Thr Glu Tyr Gln Asn Asn Lys Asn Ser Leu Glu
100 105 110

Ile Leu Leu Gly Ser Ile Gly Arg Ser Leu Pro His Ile Thr Asp Val
115 120 125

Ser Trp Arg Leu Glu Tyr Gln Ile Lys Thr Asn Gln Leu His Arg Met
130 135 140

Tyr Arg Pro Ala Tyr Leu Val Thr Leu Ser Val Gln Asn Thr Asp Ser
145 150 155 160

Pro Ser Tyr Pro Glu Ile Ser Phe Ser Cys Ser Met Glu Gln Leu Gln
165 170 175

Asp Leu Val Gly Lys Leu Lys Asp Ala Ser Lys Ser Leu Glu Arg Ala
180 185 190

Thr Gln Leu Xaa
195

<210> 129
<211> 49
<212> PRT
<213> Homo sapiens

<400> 129
Met Ala Ser Ile Leu Leu Leu Val Leu Ser His Ser Cys Cys Cys
1 5 10 15

Lys Asn Thr Cys Leu Gln Val Leu Cys Asn Phe Asp Ser Val His Asn
20 25 30

Leu Ser Thr Leu Ile Leu Lys Ile Ile Ile Arg Val Asp Val Leu Val
35 40 45

Tyr

<210> 130
<211> 55
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (55)
<223> Xaa equals stop translation

<400> 130
Met Val Tyr Cys Val His Leu Asn Pro Phe Thr Asp Leu Cys Cys Ile
1 5 10 15

Phe Phe Met Pro Leu Leu Cys Phe Leu Leu Arg Ser Arg Val Asp Ser
20 25 30

Ile Ser Ile Pro Ser Leu Thr Leu Leu Glu Ala Cys Asn Ser Ile Tyr
35 40 45

Cys Ser Gly Ser Ser Ala Xaa
50 55

<210> 131

<211> 33

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (33)

<223> Xaa equals stop translation

<400> 131

Met Gly Val Asn Lys Val Leu Phe Thr Phe Phe Phe Phe Ser Ser Leu
1 5 10 15

Leu Asp Gly Val Gly Thr Ser His Ser Leu Ala Ser Phe Pro His Thr
20 25 30

Xaa

<210> 132

<211> 24

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (24)

<223> Xaa equals stop translation

<400> 132

Met Trp Pro Leu Leu Leu Arg Leu Leu Phe Leu His Leu Phe Leu Ala
1 5 10 15

Lys Asn Lys Leu Ile Phe Lys Xaa
20

<210> 133

<211> 220

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (68)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE
 <222> (87)
 <223> Xaa equals any of the naturally occurring L-amino acids

 <220>
 <221> SITE
 <222> (98)
 <223> Xaa equals any of the naturally occurring L-amino acids

 <220>
 <221> SITE
 <222> (220)
 <223> Xaa equals stop translation

 <400> 133
 Met Ala Glu Ile His Thr Pro Tyr Ser Ser Leu Lys Lys Leu Leu Ser
 1 5 10 15
 Leu Leu Asn Gly Phe Val Ala Val Ser Gly Ile Ile Leu Val Gly Leu
 20 25 30
 Gly Ile Gly Gly Lys Cys Gly Gly Ala Ser Leu Thr Asn Val Leu Gly
 35 40 45
 Leu Ser Ser Ala Tyr Leu Leu His Val Gly Asn Leu Cys Leu Val Met
 50 55 60
 Gly Cys Ile Xaa Val Leu Leu Gly Cys Ala Gly Trp Tyr Gly Ala Thr
 65 70 75 80
 Lys Glu Ser Arg Gly Thr Xaa Leu Phe Val Gly Asp Val Ala Leu Glu
 85 90 95
 His Xaa Phe Val Thr Leu Arg Lys Asn Tyr Arg Gly Tyr Asn Glu Pro
 100 105 110
 Asp Asp Tyr Ser Thr Gln Trp Asn Leu Val Met Glu Lys Leu Lys Cys
 115 120 125
 Cys Gly Val Asn Asn Tyr Thr Asp Phe Ser Gly Ser Ser Phe Glu Met
 130 135 140
 Thr Thr Gly His Thr Tyr Pro Arg Ser Cys Cys Lys Ser Ile Gly Ser
 145 150 155 160
 Val Ser Cys Asp Gly Arg Asp Val Ser Pro Asn Val Ile His Gln Lys
 165 170 175
 Gly Cys Phe His Lys Leu Leu Lys Ile Thr Lys Thr Gln Ser Phe Thr
 180 185 190
 Leu Ser Gly Ser Ser Leu Gly Ala Ala Val Ile Gln Leu Pro Gly Ile
 195 200 205
 Leu Ala Thr Leu Leu Leu Phe Ile Lys Leu Gly Xaa
 210 215 220

<210> 134
 <211> 303
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (303)
 <223> Xaa equals stop translation

<400> 134
 Met Ile Gly Ile Ser Ala Ser Phe Ser Ala Leu Leu Glu Gln Ile Leu
 1 5 10 15

 Cys Ala Ser Gly His Ser Ser Gly Phe Ser Gly Leu Cys Gly Ala Leu
 20 25 30

 Phe Ile Thr Phe Gly Ile Leu Gly Ala Leu Ala Leu Gly Pro Tyr Val
 35 40 45

 Asp Arg Thr Lys His Phe Thr Glu Ala Thr Lys Ile Gly Leu Cys Leu
 50 55 60

 Phe Ser Leu Ala Cys Val Pro Phe Ala Leu Val Ser Gln Leu Gln Gly
 65 70 75 80

 Gln Thr Leu Ala Leu Ala Ala Thr Cys Ser Leu Leu Gly Leu Phe Gly
 85 90 95

 Phe Ser Val Gly Pro Val Ala Met Glu Leu Ala Val Glu Cys Ser Phe
 100 105 110

 Pro Val Gly Glu Gly Ala Ala Thr Gly Met Ile Phe Val Leu Gly Gln
 115 120 125

 Ala Glu Gly Ile Leu Ile Met Leu Ala Met Thr Ala Leu Thr Val Arg
 130 135 140

 Arg Ser Glu Pro Ser Leu Ser Thr Cys Gln Gln Gly Glu Asp Pro Leu
 145 150 155 160

 Asp Trp Thr Val Ser Leu Leu Leu Met Ala Gly Leu Cys Thr Phe Phe
 165 170 175

 Ser Cys Ile Leu Ala Val Phe Phe His Thr Pro Tyr Arg Arg Leu Gln
 180 185 190

 Ala Glu Ser Gly Glu Pro Pro Ser Thr Arg Asn Ala Val Gly Gly Ala
 195 200 205

 Asp Ser Gly Pro Gly Val Asp Arg Gly Gly Ala Gly Arg Ala Gly Val
 210 215 220

 Leu Gly Pro Ser Thr Ala Thr Pro Glu Cys Thr Ala Arg Gly Ala Ser
 225 230 235 240

 Leu Glu Asp Pro Arg Gly Pro Gly Ser Pro His Pro Ala Cys His Arg
 245 250 255

Ala Thr Pro Arg Ala Gln Gly Pro Ala Ala Thr Asp Ala Pro Ser Arg
260 265 270
Pro Gly Arg Leu Ala Gly Arg Val Gln Ala Ser Arg Phe Ile Asp Pro
275 280 285
Ala Gly Ser His Ser Ser Phe Ser Ser Pro Trp Val Ile Thr Xaa
290 295 300

<210> 135
<211> 41
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (41)
<223> Xaa equals stop translation

<400> 135
Met Arg Leu Val Pro Ser His Leu Leu Ala Ile Leu Ile Asn Ile Lys
1 5 10 15

Asp Gln Met Met Cys Phe Cys Ile Ala Leu Met Met Arg Leu Ser Ser
20 25 30

Cys Ile Ala Ser Ser Gly Pro Trp Xaa
35 40

<210> 136
<211> 278
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (278)
<223> Xaa equals stop translation

<400> 136
Met Ser Phe Asn Leu Gln Ser Ser Lys Lys Leu Phe Ile Phe Leu Gly
1 5 10 15

Lys Ser Leu Phe Ser Leu Leu Glu Ala Met Ile Phe Ala Leu Leu Pro
20 25 30

Lys Pro Arg Lys Asn Val Ala Gly Glu Ile Val Leu Ile Thr Gly Ala
35 40 45

Gly Ser Gly Leu Gly Arg Leu Leu Ala Leu Gln Phe Ala Arg Leu Gly
50 55 60

Ser Val Leu Val Leu Trp Asp Ile Asn Lys Glu Gly Asn Glu Glu Thr
65 70 75 80

Cys Lys Met Ala Arg Glu Ala Gly Ala Thr Arg Val His Ala Tyr Thr
85 90 95

Cys Asp Cys Ser Gln Lys Glu Gly Val Tyr Arg Val Ala Asp Gln Val
100 105 110

Lys Lys Glu Val Gly Asp Val Ser Ile Leu Ile Asn Asn Ala Gly Ile
115 120 125

Val Thr Gly Lys Lys Phe Leu Asp Cys Pro Asp Glu Leu Met Glu Lys
130 135 140

Ser Phe Asp Val Asn Phe Lys Ala His Leu Trp Thr Tyr Lys Ala Phe
145 150 155 160

Leu Pro Ala Met Ile Ala Asn Asp His Gly His Leu Val Cys Ile Ser
165 170 175

Ser Ser Ala Gly Leu Ser Gly Val Asn Gly Leu Ala Asp Tyr Cys Ala
180 185 190

Ser Lys Phe Ala Ala Phe Gly Phe Ala Glu Ser Val Phe Val Glu Thr
195 200 205

Phe Val Gln Lys Gln Lys Gly Ile Lys Thr Thr Ile Val Cys Pro Phe
210 215 220

Phe Ile Lys Thr Gly Met Phe Glu Gly Cys Thr Thr Gly Cys Pro Ser
225 230 235 240

Leu Leu Pro Ile Leu Glu Pro Lys Tyr Ala Val Glu Lys Ile Val Glu
245 250 255

Ala Ile Leu Gln Glu Lys Met Tyr Leu Tyr Met Pro Lys Val Val Ile
260 265 270

Leu His Asp Val Ser Xaa
275

<210> 137

<211> 111

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (111)

<223> Xaa equals stop translation

<400> 137

Met Leu Thr Phe Leu Met Leu Val Arg Leu Ser Thr Leu Cys Pro Ser
1 5 10 15

Ala Val Leu Gln Arg Leu Asp Arg Leu Val Glu Pro Leu Arg Ala Thr
20 25 30

Cys Thr Thr Lys Val Lys Ala Asn Ser Val Lys Gln Glu Phe Glu Lys

35 40 45
 Gln Asp Glu Leu Lys Arg Ser Ala Met Arg Ala Val Ala Ala Leu Leu
 50 55 60
 Thr Ile Pro Glu Ala Glu Lys Ser Pro Leu Met Ser Glu Phe Gln Ser
 65 70 75 80
 Gln Ile Ser Ser Asn Pro Glu Leu Ala Ala Ile Phe Glu Ser Ile Gln
 85 90 95
 Lys Asp Ser Ser Ser Thr Asn Leu Glu Ser Met Asp Thr Ser Xaa
 100 105 110

<210> 138

<211> 133

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (133)

<223> Xaa equals stop translation

<400> 138

Met Arg Ala Leu His Phe Ser Ser Arg His Asn Lys Asp Ile Ala Leu
 1 5 10 15

Val Asn Leu Ala Asn Val Leu His Arg Ala His Phe Ser Ala Asp Ala
 20 25 30

Ala Val Val Val His Ala Ala Leu Asp Asp Ser Asp Phe Phe Thr Ser
 35 40 45

Tyr Tyr Thr Leu Gly Asn Ile Tyr Ala Met Leu Gly Glu Tyr Asn His
 50 55 60

Ser Val Leu Cys Tyr Asp His Ala Leu Gln Ala Arg Pro Gly Phe Glu
 65 70 75 80

Gln Ala Ile Lys Arg Lys His Ala Val Leu Cys Gln Gln Lys Leu Glu
 85 90 95

Gln Lys Leu Glu Ala Gln His Arg Ser Leu Gln Arg Thr Leu Asn Glu
 100 105 110

Leu Lys Glu Tyr Gln Lys Gln His Asp His Tyr Leu Arg Pro Gly Asn
 115 120 125

Pro Arg Lys Thr Xaa
 130

<210> 139

<211> 131

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (131)

<223> Xaa equals stop translation

<400> 139

Met Glu Thr Leu Gly Ala Leu Leu Val Leu Glu Phe Leu Leu Leu Ser
1 5 10 15

Pro Val Glu Ala Gln Gln Ala Thr Glu His Arg Leu Lys Pro Trp Leu
20 25 30

Val Gly Leu Ala Ala Val Val Gly Phe Leu Phe Ile Val Tyr Leu Val
35 40 45

Leu Leu Ala Asn Arg Leu Trp Cys Ser Lys Ala Arg Ala Glu Asp Glu
50 55 60

Glu Glu Thr Thr Phe Arg Met Glu Ser Asn Leu Tyr Gln Asp Gln Ser
65 70 75 80

Glu Asp Lys Arg Glu Lys Lys Glu Ala Lys Glu Lys Glu Glu Lys Arg
85 90 95

Lys Lys Glu Lys Lys Thr Ala Lys Glu Gly Glu Ser Asn Leu Gly Leu
100 105 110

Asp Leu Glu Glu Lys Glu Pro Gly Asp His Glu Arg Ala Lys Ser Thr
115 120 125

Val Met Xaa
130

<210> 140

<211> 106

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (106)

<223> Xaa equals stop translation

<400> 140

Met Thr His Arg Arg His Cys Gly Leu Ala Arg Trp Ile Leu Met Lys
1 5 10 15

Ile Phe Cys Trp Arg Val Ser Thr Val Thr Ser Thr Ala Gly Ala Leu
20 25 30

Thr Asn Pro His Ser Cys Tyr Thr Ser Val Leu Lys Val Gly Ala Thr
35 40 45

Gly Val Gly Gln Ser Leu Ser Val Trp Thr Met Pro Gly Leu Leu Leu
50 55 60

Glu Gln Phe Ser Thr Gly Val Glu Leu Leu Leu Ser Ser Ser Arg Phe
 65 70 75 80

Ser Asn Ser Met Glu Tyr Lys Asn Arg Leu Ser Ser Val Glu Asp Arg
 85 90 95

Ser Ser Val Val Thr Cys Leu Lys Ala Xaa
 100 105

<210> 141

<211> 62

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (62)

<223> Xaa equals stop translation

<400> 141

Met Pro Leu Ala Leu Leu Ala Thr Trp Leu Ser Cys Leu Pro Ser Leu
 1 5 10 15

Val Leu Thr Tyr Tyr Ser Arg Ser Asn Gln Lys Met Pro Trp Thr Leu
 20 25 30

Ala Ser Pro Phe Ser Ser Met Ala Ser Thr Met Glu Phe Trp Asn Gly
 35 40 45

Thr Leu Gln Lys Cys Val Gln Thr Thr Trp His Leu Pro Xaa
 50 55 60

<210> 142

<211> 38

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (38)

<223> Xaa equals stop translation

<400> 142

Met Lys Ala Thr Leu Lys Leu Leu Pro Thr Ile Val Val Ile Tyr Cys
 1 5 10 15

Leu Leu Cys Pro Val Pro Arg Gln Ile Leu Gly Val Pro Ser Trp Ala
 20 25 30

Pro Gly Lys Cys Leu Xaa
 35

<210> 143

<211> 64

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (64)

<223> Xaa equals stop translation

<400> 143

Met Leu Thr Ser Ser Ser Asn Leu Ile Ser Trp Val Leu Pro Glu Leu
1 5 10 15

Ser Ser Leu Leu Trp Val Phe Leu Phe Trp Lys Arg Gln Cys Gly Asp
20 25 30

Trp Ala Gly Arg Lys Thr Arg Ser Arg Val Ser Gly Val Val Thr Asn
35 40 45

Phe Pro Leu His Ser Pro Ser Leu Arg Tyr Ser Ser Phe Leu Glu Xaa
50 55 60

<210> 144

<211> 105

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (105)

<223> Xaa equals stop translation

<400> 144

Met Leu Phe Cys Ile Leu Leu Tyr Thr Leu Gly Ser Ala Arg Cys His
1 5 10 15

His Leu Ser Phe Phe Leu Trp Gly Trp Ser Asn Pro Pro Glu Lys Thr
20 25 30

Pro Leu Ala Ser Trp Arg Gly Val Lys Ala Arg Leu Pro Gly Pro Gly
35 40 45

Cys Gln Leu Leu Gly Ala Ala Gly Ala Glu Ala Gly Ser Cys Gln Ala
50 55 60

Phe Ser Gln Gln Asp Ala Leu Ser Thr His Leu Gly Phe Arg Ile Pro
65 70 75 80

Leu Pro His Leu Gln Met Gly Gln Met Ser Pro Lys Pro Ala Ala Pro
85 90 95

Phe Cys Phe Thr Leu Ser Thr Glu Xaa
100 105

<210> 145

<211> 61
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (61)
<223> Xaa equals stop translation

<400> 145
Met Gly Pro Trp Cys Leu Thr Leu Leu Ser Thr Thr Ser Gly Phe Phe
1 5 10 15
Ser Glu Asn Leu Tyr Leu Thr Leu Ile Leu Ser Phe Leu Leu Ser Ile
20 25 30
Glu Ser Val Asn Thr Asp Pro Phe Ile Phe Gln Phe Pro Lys Ser Cys
35 40 45
Phe Ala Ile Ala Ser Ile Leu Leu Ser Gly Gly Val Xaa
50 55 60

<210> 146
<211> 37
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (37)
<223> Xaa equals stop translation

<400> 146
Met Gly Cys Thr Ala Leu Leu Leu Leu Phe His Leu Cys Val Pro Cys
1 5 10 15
Glu Pro Tyr Gly Thr His Glu Lys Glu Leu Val Pro Gly Leu Tyr Phe
20 25 30
Leu Val Tyr Arg Xaa
35

<210> 147
<211> 32
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (32)
<223> Xaa equals stop translation

<400> 147
Met Cys Lys Phe Ile Tyr Val Pro His Ser Val Leu Leu Val Tyr Val
1 5 10 15

Phe Thr Phe Val Leu Ile Pro Asn Cys Tyr Asn Ser Val Ala Leu Xaa
20 25 30

<210> 148

<211> 16

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (16)

<223> Xaa equals stop translation

<400> 148

Met Ser Leu Ala Leu Cys Leu Val Pro Leu Val Arg Glu Gly His Xaa
1 5 10 15

<210> 149

<211> 59

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (59)

<223> Xaa equals stop translation

<400> 149

Met Ile Ile Ser Ser Ile Arg Cys Leu Val Leu Gly Ile Glu Cys Val
1 5 10 15

Ser Ala Val Cys Gln Asn Leu Leu Leu Gly Glu Phe Pro His Trp Glu
20 25 30

Arg Asp Pro Gly Asn Gly Met Val Leu Glu Gly Leu Leu Asn Thr Phe
35 40 45

Pro Trp Glu Gly Ser Cys Tyr Leu Gln Gly Xaa
50 55

<210> 150

<211> 87

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (87)

<223> Xaa equals stop translation

<400> 150

Met Leu Lys Thr Trp Phe Phe Val Met Ala Val Ile Gly Val Ile Ile
 1 5 10 15

Pro Thr Val Phe Asp Gln Ser Ser Arg Leu Cys Leu Lys Glu Thr Gly
 20 25 30

Phe Val Gln Asn Val Asp Gln Ser Asn Val Leu Glu Asp Ser Pro Leu
 35 40 45

Asp Arg Asp His Pro Trp Lys Val Met Lys Met Trp Lys Thr Val Trp
 50 55 60

Glu Val Arg Met Met Lys Leu Met Ala Met Lys Lys Lys Val Lys Val
 65 70 75 80

Arg Arg Lys Ser Met Arg Xaa
 85

<210> 151

<211> 53

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (51)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (53)

<223> Xaa equals stop translation

<400> 151

Met Asp Ile Cys Ser Pro Val Ala Leu Tyr Phe Leu Leu Thr Ala Ala
 1 5 10 15

His Ile Thr Ala Val Ser Lys Pro Thr Val Met Leu Arg Glu Arg Pro
 20 25 30

Cys Ser Gly Pro Ser Arg Ser Ala Pro Gln Ser Arg Leu Ile Gly Pro
 35 40 45

Trp Asp Xaa Cys Xaa
 50

<210> 152

<211> 78

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (78)

<223> Xaa equals stop translation

<400> 152

Met Ala Leu Lys Asn Lys Phe Ser Cys Leu Trp Ile Leu Gly Leu Cys
1 5 10 15
Leu Val Ala Thr Thr Ser Ser Lys Ile Pro Ser Ile Thr Asp Pro His
20 25 30
Phe Ile Asp Asn Cys Ile Glu Ala His Asn Glu Trp Arg Gly Lys Val
35 40 45
Asn Pro Pro Ala Ala Asp Met Lys Tyr Met Ile Trp Asp Lys Gly Leu
50 55 60
Ala Lys Met Ala Lys Ala Trp Gly Lys Pro Val Gln Ile Xaa
65 70 75

<210> 153

<211> 72

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (72)

<223> Xaa equals stop translation

<400> 153

Met Leu Gln Ala Ala Ser Leu Ser Leu Val Thr Trp Val Val Cys Thr
1 5 10 15
Val Trp Leu Glu Thr Thr Val Pro Pro Ser Leu Pro Glu Pro Pro Met
20 25 30
Trp Pro Leu Ser Ser Asp Ser Ser Trp Ser Leu Trp Ile Ser Thr Gly
35 40 45
Met Ala Pro Ala Pro Ser Ser Ser Thr Arg Ser Phe Ser Val Leu Pro
50 55 60
Glu Ile Cys Phe Cys Leu Trp Xaa
65 70

<210> 154

<211> 41

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (41)

<223> Xaa equals stop translation

<400> 154

Met Leu Gln Glu Val Lys Leu Asp Phe Leu Trp Leu Leu Asn Leu Pro

Arg His Met Val Phe Thr His Gly Leu Trp Ala Leu Glu Lys Leu Ser
 50 55 60

Pro Leu Lys Glu Asn Gln Asn Val Ala Cys Ile Cys Ile Phe Cys Leu
 65 70 75 80

Arg Phe His Leu Ile Leu Lys Trp Ile Leu Asp Ser Pro Lys Val Xaa
 85 90 95

<210> 157
 <211> 89
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (89)
 <223> Xaa equals stop translation

<400> 157
 Met Trp Ala Val Leu Pro Ala Trp Phe Pro Phe Pro Gly Thr Cys His
 1 5 10 15

Cys Leu Pro Val Ser Leu Arg Gly His Phe Trp Glu Val Arg Pro Trp
 20 25 30

Pro Pro Gly Pro Leu Phe Arg Ser Glu Ala Pro Thr Cys Leu Gly Ser
 35 40 45

Gly Ser Ser Gly Val Arg Pro Cys Pro Pro Gln Asp Ile Pro Ser Lys
 50 55 60

Pro Ala Met Ser Gly Asp Gly Pro Leu Pro Gly Lys Val Leu Phe Leu
 65 70 75 80

Leu Val Thr Glu Lys Asn Leu Pro Xaa
 85

<210> 158
 <211> 44
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (44)
 <223> Xaa equals stop translation

<400> 158
 Met Ser Ala Leu Ser Phe Thr Ser Tyr Phe Leu Leu Leu Leu Arg Val
 1 5 10 15

Lys Pro Val Glu Val Ser Gly Ser Ile Pro His Pro Glu Gln Pro Asn
20 25 30

Val Leu Cys Leu Val Leu Pro Thr Phe Gly Tyr Xaa
35 40

<210> 159

<211> 46

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (46)

<223> Xaa equals stop translation

<400> 159

Met Cys Cys Phe Phe Leu Lys Thr Leu Asn Leu Trp Leu Gly Tyr Phe
1 5 10 15

Cys Gln Phe Ile Cys Leu Pro Cys Gln Val Thr Leu Cys Leu Ile Asp
20 25 30

Val Leu Cys Val Phe His Ser Val His Ala Glu Leu Ser Xaa
35 40 45

<210> 160

<211> 62

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (62)

<223> Xaa equals stop translation

<400> 160

Met Tyr Leu Phe Leu Lys Thr Leu Leu Ser Phe Ser Thr Leu Met Met
1 5 10 15

Thr Thr Ala Leu Ser Phe Met Val Ile Thr Val Leu Trp Val Leu Leu
20 25 30

Leu His Leu Leu Ala Asn Ile Cys Ile Pro Arg Lys Cys Ser Phe Ala
35 40 45

Cys Phe Tyr Ile Asn Gly Ile Leu Leu His Ala Val Phe Xaa
50 55 60

<210> 161

<211> 31

<212> PRT

<213> Homo sapiens

<220>

<221> SITE
<222> (31)
<223> Xaa equals stop translation

<400> 161

Met Val Ser Leu Leu Ser Leu Thr Phe His Gln Phe Val Ser Ser Leu
1 5 10 15
Lys Tyr Phe Lys Leu Leu Ser Thr Ser Arg Gln Glu Ile Leu Xaa
20 25 30

<210> 162
<211> 25
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (25)
<223> Xaa equals stop translation

<400> 162

Met Ala Gly Asn Gln Gln Phe Val Asn Leu Leu Leu Arg Ser Val Ile
1 5 10 15
His Ser Val Ala Tyr Phe Leu Ser Xaa
20 25

<210> 163
<211> 71
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (71)
<223> Xaa equals stop translation

<400> 163

Met Glu Asn Pro Thr Ser Thr Pro Thr Leu Pro Cys Phe Leu Phe Phe
1 5 10 15
Phe Ser Pro Arg Ser Leu Asp Val Leu Thr Pro Pro His Cys Leu Leu
20 25 30
Ser Gly Thr Gly Trp Asp Leu Glu Glu Asp Lys Ala Phe Leu Asp Tyr
35 40 45
Pro Ser Tyr Ser Val Ser Leu Phe Leu Thr Gln Arg Gly Arg Gln Asn
50 55 60
Gln Ser Gly Leu Phe Gln Xaa
65 70

<210> 164

<211> 43
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (43)
<223> Xaa equals stop translation

<400> 164
Met Arg Ile His Pro Ile Phe Arg Leu Gly Asn Val Tyr Ser Leu Leu
1 5 10 15
Ser Phe Leu Ile Leu Gly Arg Val Ser Thr Lys Asn Ser Ile Glu Glu
20 25 30
Lys Gln Tyr Asn Ile Lys Ile Lys Lys Ile Xaa
35 40

<210> 165
<211> 65
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (65)
<223> Xaa equals stop translation

<400> 165
Met Glu Lys Leu Leu Thr Leu Tyr Leu Leu Leu Tyr Val Ser Tyr Trp
1 5 10 15
Ser Val Ser Pro Thr Gly Gln Gly Ala Gly Leu Phe Ile Ala Gln Ser
20 25 30
Ser Ala Pro Gly Leu Arg Gln Thr His Ser Arg His Leu Gly Asn Ala
35 40 45
Trp Glu Arg Lys Glu Gly Arg Arg Glu Glu Gly Leu His Gly His Val
50 55 60
Xaa
65

<210> 166
<211> 68
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (68)
<223> Xaa equals stop translation

<400> 166

Met Leu Phe Ser Leu Pro Arg Thr Phe Ser Ser His Ser Ser Pro Ala
1 5 10 15
Gln Leu Ile Phe Ile His Ala Ala Ser Val Leu Met Ala Phe Pro Pro
20 25 30
Arg Pro Ser Lys Thr Thr Leu Pro Gln Ala Ala Phe Leu Thr Ser Leu
35 40 45
Ala Cys Pro Leu Met Leu Ser Thr Phe Phe Leu Tyr Gln Asn Ala Phe
50 55 60
Val Cys Lys Xaa
65

<210> 167
<211> 59
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (59)
<223> Xaa equals stop translation

<400> 167
Met Ser Ser Phe Pro Gly Pro Gln Cys Val Gln Leu Ile Asn Leu Leu
1 5 10 15
His Leu Ile Cys Pro Val Ser Gly Leu Val Cys Ser Ala Ile Thr Ile
20 25 30
Ala Leu Arg Gln Lys Ser Ile Pro His Gln Gln Gly Arg Glu Ala Val
35 40 45
Ile Lys Thr Pro Pro Pro Gly Ser Leu Pro Xaa
50 55

<210> 168
<211> 54
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (30)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (34)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (38)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (54)

<223> Xaa equals stop translation

<400> 168

Met Leu Val Leu Ala Trp Ile Thr Phe Pro Pro Cys Lys Ala Cys Cys
1 5 10 15

Met Met Cys Ile Phe Ser Ser Arg Leu Leu Gln Gln Glu Xaa Val Cys
20 25 30

Thr Xaa Val Gln Gly Xaa Glu Pro Arg Gly Met Ala Gln Arg Asp Arg
35 40 45

Gly Phe Glu Ser Leu Xaa
50

<210> 169

<211> 20

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (20)

<223> Xaa equals stop translation

<400> 169

Met Val Tyr His Gly Tyr Asn Ile Tyr Leu Val Val Phe Leu Leu Leu
1 5 10 15

Tyr Leu Asp Xaa
20

<210> 170

<211> 39

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (39)

<223> Xaa equals stop translation

<400> 170

Met Gly Pro Ala Val Cys Phe Arg Ala Cys Glu Met Cys Ser Leu Ser
1 5 10 15

Gly Leu Leu Leu Asn Leu Cys Phe Gln Ser Cys Leu Ser Val Pro Leu
20 25 30

Ser Gly Val Pro Arg Val Xaa
35

<210> 171
 <211> 54
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (54)
 <223> Xaa equals stop translation

<400> 171
 Met Asn Leu Glu Thr Val Leu Leu Ser Arg Thr Ser Ser Leu Gly Phe
 1 5 10 15
 Ala Val Cys Leu Pro Cys Phe Phe Cys Trp Phe Tyr Leu Val Leu Phe
 20 25 30
 Leu Glu Leu Thr Ser Ile Thr Phe Ala Met Tyr Asp Ile Ile Pro Cys
 35 40 45
 Met Thr Leu Gly Lys Xaa
 50

<210> 172
 <211> 55
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (55)
 <223> Xaa equals stop translation

<400> 172
 Met Ser Trp Ala Leu Pro Ser Leu Phe Phe Leu Leu Phe Ser Pro Phe
 1 5 10 15
 Leu Leu Pro Ser Gly Leu Thr Val Ile Arg Arg Tyr Thr Asn Asn Ser
 20 25 30
 Asn Asn Tyr Leu Lys Asn His Thr His Gln Lys Asn Lys Arg Gln Gln
 35 40 45
 Lys Ile Thr Arg Tyr Ser Xaa
 50 55

<210> 173
 <211> 47
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (47)

<223> Xaa equals stop translation

<400> 173

Met Leu Ser Pro Leu Asn His Leu Tyr Phe Pro Phe Arg Phe Leu Cys
1 5 10 15

Met Leu Cys Ser Leu Pro Arg Val Val Phe Gln Leu Thr Pro Ile Lys
20 25 30

Glu Ala Phe Pro Ser Gln Glu Leu Thr Phe Pro Cys Thr His Xaa
35 40 45

<210> 174

<211> 55

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (55)

<223> Xaa equals stop translation

<400> 174

Met Leu Leu Gly Phe Leu Cys Leu Trp Tyr Gln Val Tyr Val Cys Met
1 5 10 15

Tyr Val Cys Thr Tyr Leu Phe Ile Tyr Leu Leu Phe Ser Leu Phe Ser
20 25 30

Leu Pro His Met Ile Cys Lys Lys Ser Val Lys Phe Ile Met Ser Ser
35 40 45

Pro Lys Pro Pro Ser Gly Xaa
50 55

<210> 175

<211> 27

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (27)

<223> Xaa equals stop translation

<400> 175

Met Lys Trp Ser Leu Leu Lys Val Val Leu Val Phe Val Phe Val Cys
1 5 10 15

Gly Phe Leu Lys Arg Ala Tyr Pro Ala Thr Xaa
20 25

<210> 176

<211> 50

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (50)

<223> Xaa equals stop translation

<400> 176

Met Ile Asp Ile Cys His Ser Leu Arg Arg Glu His Phe Leu Leu Trp
1 5 10 15

Ser Phe Leu Gly Leu Phe Tyr Trp Ala Val Asn Gly Lys Ser Val Cys
20 25 30

Val Ser Leu Leu His Pro Lys His Leu Gly Lys Asn Glu Ser Leu Leu
35 40 45

Ile Xaa
50

<210> 177

<211> 27

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (27)

<223> Xaa equals stop translation

<400> 177

Met Phe His Ser Ser Leu Leu Val Phe Leu Ser Leu Leu Ser Gln Glu
1 5 10 15

Ile Phe Thr Glu Tyr Asp Cys Met His Lys Xaa
20 25

<210> 178

<211> 41

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (41)

<223> Xaa equals stop translation

<400> 178

Met Val His Val Ser Asn Leu Pro Trp Cys Leu Met Thr Leu Ser Ile
1 5 10 15

Phe Ala Leu Leu Cys Asn His His Cys His Pro Ser Thr Glu Arg Leu
20 25 30

Ser Ser Cys Lys Thr Glu Thr Pro Xaa
35 40

<210> 179
<211> 65
<212> PRT
<213> Homo sapiens

<400> 179
Met Ile Trp Arg Leu Ser Asp Asn Ser Ala Leu Ile Leu Leu Cys Leu
1 5 10 15
Gln Asn Leu Cys Trp Pro Thr Trp Met Ala Gly Glu Asp Gln Gln Lys
20 25 30
Val Pro Ser Thr His Val Leu Pro Ala Leu Thr Leu Val Ser Leu Gly
35 40 45
Ala Asn Ser Cys Arg Ile Arg Tyr Gln Ala Tyr Arg Tyr Arg Arg Pro
50 55 60
Arg
65

<210> 180
<211> 20
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (20)
<223> Xaa equals stop translation

<400> 180
Met Val Gly Thr Trp Arg Met Leu Phe Leu Leu Pro Ser Tyr Ser Ser
1 5 10 15
Gly Gln Val Xaa
20

<210> 181
<211> 15
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (15)
<223> Xaa equals stop translation

<400> 181
Met Trp Asp Tyr Lys Thr Val Leu Leu Ala Phe Lys Gln Leu Xaa
1 5 10 15

<210> 182

<211> 46
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (46)
<223> Xaa equals stop translation

<400> 182
Met Val Lys Trp Ile Ile Leu Ser Cys Leu Ile Leu Lys Gly Lys Arg
1 5 10 15
Thr Leu Asn Ser Ser Thr Phe Tyr Ala Ala Asn Lys Ser Ser Thr Ile
20 25 30
Asn Arg Asn Leu Ser Trp Gln Ala Leu Pro Phe Thr His Xaa
35 40 45

<210> 183
<211> 72
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (19)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (22)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (57)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (70)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (72)
<223> Xaa equals stop translation

<400> 183
Met Ser Leu Leu Leu Pro Pro Leu Ala Leu Leu Leu Leu Ala Ala
1 5 10 15
Leu Val Xaa Pro Ala Xaa Ala Ala Thr Ala Tyr Arg Pro Asp Trp Asn
20 25 30
Arg Leu Ser Gly Leu Thr Arg Ala Arg Val Glu Thr Cys Gly Gly Met

35 40 45
 Thr Ala Glu Pro Pro Lys Gly Glu Xaa Arg Leu Ser Ser Arg Arg Thr
 50 55 60

Phe His Ser Ile Thr Xaa Trp Xaa
 65 70

<210> 184
 <211> 78
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (78)
 <223> Xaa equals stop translation

<400> 184
 Met Gly Leu Trp Phe Pro Met Leu Ile Leu Thr Gln Arg Phe Val Ser
 1 5 10 15

Cys Asp Ser His Pro Asp Pro Lys His Thr His Thr His Ala His Ile
 20 25 30

Asn Thr His Thr His Arg His Val His Thr Gln Thr His Met His Thr
 35 40 45

His Ile His Thr Pro Trp Phe Glu Glu Lys Arg Asp Gly Asn Arg His
 50 55 60

Ser Thr His Ala Tyr Ser Ala Pro Leu Cys Ile Gly Asn Xaa
 65 70 75

<210> 185
 <211> 26
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (26)
 <223> Xaa equals stop translation

<400> 185
 Met Leu Asn Lys Cys Gln Thr Ile Phe Tyr Ile Thr Leu Leu Leu Phe
 1 5 10 15

Asn Phe Val Thr Phe Arg Gly Gly Gly Xaa
 20 25

<210> 186
 <211> 63
 <212> PRT
 <213> Homo sapiens

<220>

<221> SITE

<222> (63)

<223> Xaa equals stop translation

<400> 186

Met Glu Asn Val Cys Gln Ala Gly Phe Pro Ser Leu Leu His Leu Asn
1 5 10 15

Ile Thr Leu Thr Leu Leu Gly Leu Ala Gln Cys Tyr Leu Ala Asn Phe
20 25 30

Ser Ser Cys Arg Glu Gly Ser Glu His Tyr Leu Phe Phe Phe Phe
35 40 45

Leu Leu Glu Pro Gly Leu His Lys Ala Met Ala Lys Phe Ser Xaa
50 55 60

<210> 187

<211> 92

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (92)

<223> Xaa equals stop translation

<400> 187

Met Cys Pro Leu His Val Pro Leu Pro Gly His Met Gly Pro Phe Trp
1 5 10 15

Pro Leu Pro Ser Leu Tyr Ser Val Arg Ser Ser Gln Ser Pro Cys Pro
20 25 30

Leu Cys Phe Ser Leu Leu Pro Leu Gln Ala His Leu Ser Leu Leu His
35 40 45

Thr Leu Phe Arg Ser Ala Ser Gln Ser Pro Ala Ser Gly Val Phe Trp
50 55 60

Gly Cys Leu Arg Glu Arg His Glu Tyr Met Ser Pro Cys Leu Pro His
65 70 75 80

Met Tyr Gln Lys Phe Asp Phe Phe Phe Phe Xaa
85 90

<210> 188

<211> 48

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (48)

<223> Xaa equals stop translation

<400> 188

Met Ala Pro Pro Arg Gly Thr Trp Phe Leu Leu Leu Ser Leu Arg Leu
1 5 10 15
Pro Tyr Gly Ala Ala Cys Trp Val Phe Leu Pro Phe Pro Ala Ser Cys
20 25 30
Arg Ala Glu Gly Val Ala Ala Pro Ile Lys Cys Ser Arg Asn Glu Xaa
35 40 45

<210> 189

<211> 45

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (45)

<223> Xaa equals stop translation

<400> 189

Met Cys Leu Gly His Ala Phe Cys Leu Leu Leu Ser His Ser Cys Arg
1 5 10 15
Met His Cys Thr Cys Tyr Leu Cys Leu Phe Thr Val Gln Val Leu Pro
20 25 30
Gly Lys Tyr Asn Glu Gly Gly Glu Gly Gln Arg Asn Xaa
35 40 45

<210> 190

<211> 48

<212> PRT

<213> Homo sapiens

<400> 190

Met Phe Pro Gly Cys Ile Leu Leu Cys Asn Leu Cys Met Phe Phe Val
1 5 10 15
Leu Ser Phe Ser Met Gly Ile Phe Ala Phe Tyr Ser Leu Ile Arg Ala
20 25 30
Met His Val Ser Arg Leu Asp Phe Asn Phe Ala Thr Tyr Phe Val Ala
35 40 45

<210> 191

<211> 82

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (2)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (74)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (82)

<223> Xaa equals stop translation

<400> 191

Met	Xaa	Glu	Gly	Gly	Arg	Cys	Gly	Tyr	Val	Leu	Leu	Pro	Val	Ser	Leu
1				5					10					15	

Leu	Gln	Cys	Leu	Ala	Met	Gly	His	Lys	His	Tyr	Pro	Ala	Val	Gly	Arg
			20					25					30		

Leu	Ala	Lys	Arg	Ser	Gln	Leu	Ala	Ser	Pro	Ala	Ser	Ser	Arg	Glu	Trp
		35					40						45		

Asn	His	Gly	Ser	Asn	Thr	Leu	Leu	Arg	Lys	Gln	Lys	Leu	Tyr	Gly	His
	50						55				60				

Ile	Phe	His	Leu	Leu	Ser	Pro	Arg	Asn	Xaa	Met	Tyr	Cys	Asp	Pro	Ala
	65				70					75					80

His Xaa

<210> 192

<211> 40

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (40)

<223> Xaa equals stop translation

<400> 192

Met	Trp	Leu	Thr	Gln	Pro	Glu	Ser	Leu	Ser	Leu	Cys	Val	Ser	Val	Ser
1				5					10					15	

Gln	Asp	Trp	Ala	His	Ile	Leu	Ala	Leu	Ser	Ile	Thr	Met	Leu	Trp	Asp
			20					25					30		

Phe	Arg	Glu	Phe	Pro	His	Leu	Xaa
		35				40	

<210> 193
 <211> 182
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (182)
 <223> Xaa equals stop translation

<400> 193
 Met Ala Ser Phe Leu Lys Gly Ile Thr Ala Thr Val Leu Ile Asn Ala
 1 5 10 15
 Cys Val Ala Asn Thr Val Ala Pro Leu His Tyr Lys Asp Met Ile Ile
 20 25 30
 Pro Lys Leu Val Asp Asp Leu Gly Lys Val Lys Ile Thr Lys Ser Gly
 35 40 45
 Phe Leu Thr Phe Met Asp Thr Trp Ser Asn Pro Leu Glu Glu His Asn
 50 55 60
 His Gln Ser Leu Val Pro Leu Glu Lys Ala Gln Val Pro Phe Leu Phe
 65 70 75 80
 Ile Val Gly Met Asp Asp Gln Ser Trp Lys Ser Glu Phe Tyr Ala Gln
 85 90 95
 Ile Ala Ser Glu Arg Leu Gln Ala His Gly Lys Glu Arg Pro Gln Ile
 100 105 110
 Ile Cys Tyr Pro Glu Thr Gly His Cys Ile Asp Pro Pro Tyr Phe Pro
 115 120 125
 Pro Ser Arg Ala Ser Val His Ala Val Leu Gly Glu Ala Ile Phe Tyr
 130 135 140
 Gly Gly Glu Pro Lys Ala His Ser Lys Ala Gln Val Asp Ala Trp Gln
 145 150 155 160
 Gln Ile Gln Thr Phe Phe His Lys His Leu Asn Gly Lys Lys Ser Val
 165 170 175
 Lys His Ser Lys Ile Xaa
 180

<210> 194
 <211> 40
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (40)
 <223> Xaa equals stop translation

<400> 194

Met Tyr Tyr Thr Ala Ala Cys Leu Phe Ile Ser Val Leu Phe Leu Gly
 1 5 10 15

Leu Ser Val Leu Ile Ser Val Ala Val Val His Ser Phe Phe Lys His
 20 25 30

Cys Ile Val Phe His Asp Asp Xaa
 35 40

<210> 195

<211> 73

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (73)

<223> Xaa equals stop translation

<400> 195

Met Ala Ile Ala Leu Gly Pro Leu Val Leu Ser Trp Leu Cys Tyr Leu
 1 5 10 15

Trp Leu Thr Leu Glu Ser Leu Cys Thr Asn Lys Met Ala Ser Asp Glu
 20 25 30

Pro Val Ser His His Cys Leu Pro Arg Leu Ser Glu Pro Pro Leu Thr
 35 40 45

Phe Cys Leu Glu Ala Gly Gly Leu Val Glu Val Gly Asp Leu Leu Lys
 50 55 60

Ser Arg Ala Arg Pro Val Ile Leu Xaa
 65 70

<210> 196

<211> 56

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (56)

<223> Xaa equals stop translation

<400> 196

Met Ala Gly His Pro Val Phe Phe Leu Leu Ile His Leu Leu Pro Leu
 1 5 10 15

Asp Phe Ser Met Gly Trp Thr Gln Thr Pro Gly Ser Asn Asn Trp Arg
 20 25 30

Arg Gly Trp Lys Glu Val Ser Gly Ser Ser Ala Pro Glu Gly Ser Arg
 35 40 45

Asp Gly Tyr Val Ala Ala Ala Xaa
50 55

<210> 197
<211> 70
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (70)
<223> Xaa equals stop translation

<400> 197
Met Ala Gly Ser Tyr Ser Ser Asp Ile Leu Val Leu Ala Arg Ser Trp
1 5 10 15
Thr Leu Leu Leu Leu Ser Val Leu Arg Leu Gln Thr Val Gly Ser Ser
20 25 30
Val Thr Leu Asp Ser Gln Val Gly Ile Ile Trp Pro Ala Val Phe Lys
35 40 45
Ile Gly Asn Arg Val Lys Lys Gln Asn Gln Ile Lys Glu Lys Arg Gln
50 55 60
Gln Gln Asn Gln Asn Xaa
65 70

<210> 198
<211> 47
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (47)
<223> Xaa equals stop translation

<400> 198
Met Trp Ile Tyr Thr Leu Thr Tyr Ile Leu Ile Asn Ser Ser Met Leu
1 5 10 15
Ala Leu Val Leu Ser Lys Leu Tyr Leu Asn Lys Phe Val Ala Arg Asn
20 25 30
Val Leu Lys Ser Tyr Ser Pro Phe Leu Leu Glu Val Ser Lys Xaa
35 40 45

<210> 199
<211> 55
<212> PRT
<213> Homo sapiens

<220>

<221> SITE

<222> (55)

<223> Xaa equals stop translation

<400> 199

Met Leu Glu Trp Pro Ile Ser Met Tyr Phe Val Ala Phe Leu His Cys
1 5 10 15

Phe Leu Cys Ser Gly Gly Asn Leu Gly Asp Ser Phe Gln Ala Leu Pro
20 25 30

Glu Leu Cys Ala Asn Cys Ser Ser Ser Pro Arg Val Leu Cys Cys Val
35 40 45

Val Met Ser Pro Leu Pro Xaa
50 55

<210> 200

<211> 38

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (38)

<223> Xaa equals stop translation

<400> 200

Met Ala Ser Glu Trp Val Gly Leu Ser Ser Leu Ile Thr Leu Leu Leu
1 5 10 15

Leu Ser Cys Val Leu Ser Cys Ile Thr Leu Glu Glu Gly Glu Lys Glu
20 25 30

Leu Val Phe Gly Pro Xaa
35

<210> 201

<211> 34

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (21)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (34)

<223> Xaa equals stop translation

<400> 201

Met Cys Leu Leu Ala His Leu Phe Cys His His Leu Leu Ile Leu Leu
1 5 10 15

Pro Val Ile Glu Xaa Leu Leu Cys Thr Arg His Trp Ala Arg Gly Ile
 20 25 30

Leu Xaa

<210> 202
 <211> 22
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (22)
 <223> Xaa equals stop translation

<400> 202
 Met Gln Leu Val Leu Phe His Arg Leu Ile Met Pro Leu Phe Phe Ala
 1 5 10 15

Arg Thr Leu Val Asp Xaa
 20

<210> 203
 <211> 56
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (56)
 <223> Xaa equals stop translation

<400> 203
 Met Lys Gln Arg Gly Glu Gln Val Pro Leu Leu Pro Pro Leu Leu
 1 5 10 15

Leu Ser Thr Arg Leu Trp Pro Cys Trp Gly Val Pro Thr Glu Ser Val
 20 25 30

Gly Ser Gly Leu Ala Arg Lys Ser Val Gly Ala Ser Gln Gly His Asn
 35 40 45

Tyr Pro Met Pro His Arg Val Xaa
 50 55

<210> 204
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 204
 Met Phe Lys Ile His Glu Lys Ser Cys Asn Pro Ile Leu Ala Tyr Leu
 1 5 10 15

Phe Leu Leu Leu Phe Gly Phe Cys Leu Ile Trp Lys Trp Thr Val Pro
 20 25 30
 Leu Leu Thr Ser Gly Arg Pro Tyr Glu Asn Leu Lys Pro Arg Gln Gly
 35 40 45
 Asp Lys Val Trp Ser Phe Ser Thr Lys Gly Arg Leu Arg Leu Leu Leu
 50 55 60
 Tyr Leu Glu Lys Gln Asn Val Val Ala Lys Asp Ser Glu Ser Gln Ile
 65 70 75 80
 Phe Phe Pro Gly Leu Ser Val Ser Glu Phe Leu Asp Phe Ser Phe Asn
 85 90 95
 Leu Ala Ile Arg Glu Phe Leu Arg Leu Glu Ile Pro Arg Gln Asn Pro
 100 105 110
 Asn Lys Ile Ser
 115

<210> 205
 <211> 84
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (84)
 <223> Xaa equals stop translation

<400> 205
 Met Lys Cys Leu Ala Pro Met Trp Val Ser Leu Trp Asp Ser Asp Pro
 1 5 10 15
 Leu Arg Ser Cys Leu Leu Leu Leu Ile Pro His Phe Ser Val Phe Leu
 20 25 30
 Ile Leu Ala Ala Val Ser Cys Leu Pro Leu Ser Thr Ala Thr Arg Trp
 35 40 45
 Arg Gly Arg Asp Pro Val Leu Leu Ile Ile Cys Leu Leu Lys Asn Leu
 50 55 60
 Gln Asn Gly Lys Ile Thr Ile Cys Ala Glu Leu Ile Ile Ser Leu Lys
 65 70 75 80
 Phe Lys Thr Xaa

<210> 206
 <211> 46
 <212> PRT
 <213> Homo sapiens

<220>

<221> SITE

<222> (46)

<223> Xaa equals stop translation

<400> 206

Met Leu Phe Ser Phe Leu Phe Thr Arg Ala Thr Pro Ala Thr Phe Leu
 1 5 10 15

Ser Leu Leu Val Arg Leu Ile Ser Ala Leu Glu His Pro Cys Cys Cys
 20 25 30

His His Leu Lys Cys Phe Ser Ser Gly Ile Leu Phe Trp Xaa
 35 40 45

<210> 207

<211> 42

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (42)

<223> Xaa equals stop translation

<400> 207

Met Ala Asn Thr Ala Arg Ile Phe Leu Leu Leu Pro Ile Phe Ile Ile
 1 5 10 15

Glu Gly Asn Ala Asn Met Lys Ile Lys Met Ser Leu Phe Pro Gln Ser
 20 25 30

Met Gln Phe Pro Pro Lys Leu Tyr Pro Xaa
 35 40

<210> 208

<211> 41

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (41)

<223> Xaa equals stop translation

<400> 208

Met Glu Thr Gln Ile Cys Leu Thr Gln Ile Val Ala Leu Phe Phe Leu
 1 5 10 15

Arg Leu Val Leu Gly Lys Leu Thr Cys Phe Leu Tyr Gly Lys Leu Val
 20 25 30

Leu Val Glu Ala Phe Ile Leu Ala Xaa
 35 40

<210> 209
 <211> 31
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (31)
 <223> Xaa equals stop translation

<400> 209
 Met Ala Ser His Cys Trp Met Gly Ala Val Cys Val Leu Phe Leu Gly
 1 5 10 15
 Ile Ile Phe Leu Ala Ala Leu Phe Pro Tyr Ile Ser Phe Tyr Xaa
 20 25 30

<210> 210
 <211> 12
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (12)
 <223> Xaa equals stop translation

<400> 210
 Met Leu Arg Ala Leu Cys Leu Ser Thr Cys Pro Xaa
 1 5 10

<210> 211
 <211> 100
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (5)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (100)
 <223> Xaa equals stop translation

<400> 211
 Met Leu Trp Tyr Xaa Phe Pro Thr Thr Pro Leu Pro Ala Gln Val Gln
 1 5 10 15
 Phe Trp Trp Cys Leu Cys Cys Cys Tyr Ile His Gly Ser Trp Trp Gly
 20 25 30
 Pro Leu Ser Gln Ser Ser Ser Ser Cys Asn Ala Ser Val Thr Ala Leu
 35 40 45

Ser Ser Gly Cys Cys Arg Pro Arg Ala Ser Ser Pro Thr Val Pro His
 50 55 60

His Arg Leu Phe Pro Met Pro Ala His Thr Ser Val Asn Ser Pro Phe
 65 70 75 80

Ile Ser His Pro Ser Val Arg Pro Phe Glu Tyr Ala Ile Cys Phe Arg
 85 90 95

Ser Gly Gln Xaa
 100

<210> 212
 <211> 29
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (3)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (29)
 <223> Xaa equals stop translation

<400> 212
 Met Leu Xaa Gln Phe Phe Leu Phe Val Cys Phe His Phe Ile Thr Tyr
 1 5 10 15

Gly Phe Leu Cys His Thr Thr Arg Asn Phe Glu Lys Xaa
 20 25

<210> 213
 <211> 47
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (47)
 <223> Xaa equals stop translation

<400> 213
 Met Gln Pro Ser Cys Val Asn Phe Arg Leu Lys Leu Phe Tyr Ser His
 1 5 10 15

Thr Phe Met Leu Arg Leu Gly Phe Leu Phe Gly Leu Leu Asp Ala His
 20 25 30

Phe Asp Ile Asp Ile Arg Gly Phe Lys Pro Ser Leu Lys Gly Xaa
 35 40 45

<210> 214

<211> 86
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (86)
<223> Xaa equals stop translation

<400> 214
Glu Leu Gln Pro Asn Pro His Ala Arg Ala Lys Pro Cys Cys Tyr Leu
1 5 10 15
Leu Phe Leu Ser Cys Leu Ile Pro Ser Met Phe Ser Leu Ser Val Asp
20 25 30
Pro Val Ser Pro Val Leu Arg Ile Val Pro Gly Ser Asp His Phe Ser
35 40 45
Leu Pro Leu Leu Leu Pro Pro Pro Leu Ala Trp Ile Ile Ala Ala Ala
50 55 60
Ser Gln Leu Ala Leu Leu Cys Pro Ser Leu Phe Ser Pro Ser Val Cys
65 70 75 80
Ser Gln Gln Arg Ser Xaa
85

<210> 215
<211> 82
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (49)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 215
Met Leu Met Lys Ile Asn Phe Tyr Pro Leu Pro Lys Pro Lys Leu His
1 5 10 15
Thr Ser Ile Ser Asn Cys Leu Leu Asp Ile Ser Ile Tyr Lys Pro Ser
20 25 30
Ser Leu Ile Ser Ile Thr Ser Asp Leu Pro Gly Leu Thr Leu Lys Ser
35 40 45
Xaa Asn Phe Ser Pro Thr Pro Met Pro Gly Gln Asn Leu Val Val Thr
50 55 60
Ser Tyr Ser Ser Leu Ala Ser Ser His Pro Cys Ser Val Cys Gln Trp
65 70 75 80
Ile Leu

<210> 216
<211> 70
<212> PRT
<213> Homo sapiens

<400> 216
Leu Ala Pro Arg Phe Ala Phe Ser Gln Cys Ser Leu Ala Ile Met Leu
1 5 10 15
Thr Leu Leu Phe Gln Ile His Phe Leu Met Ile Leu Ser Ser Asn Trp
20 25 30
Ala Tyr Leu Lys Asp Ala Ser Lys Met Gln Ala Tyr Gln Asp Ile Lys
35 40 45
Ala Lys Glu Glu Gln Glu Leu Gln Asp Ile Gln Ser Arg Ser Lys Glu
50 55 60
Gln Leu Asn Ser Tyr Thr
65 70

<210> 217
<211> 56
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (13)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 217
Ile Arg His Glu Gly Gly Gly Gln Pro Phe Thr Ser Xaa Pro Leu Glu
1 5 10 15
Ile Leu Phe Phe Leu Asn Gly Trp Tyr Asn Ala Thr Tyr Phe Leu Leu
20 25 30
Glu Leu Phe Ile Phe Leu Tyr Lys Gly Val Leu Leu Pro Tyr Pro Thr
35 40 45
Ala Asn Leu Val Leu Asp Val Val
50 55

<210> 218
<211> 89
<212> PRT
<213> Homo sapiens

<400> 218
Met Val His Thr Arg Cys Ser Gly His Gly Asp Gln Gly Gly Glu Leu
1 5 10 15
Glu Val Ser Arg Gly Leu Val Leu Arg Arg Gly Arg Met Gly Ile Thr
20 25 30

Leu Pro Leu Pro Ile Leu Glu Cys Arg Arg Val Ser Trp Ala Asp Gly
 35 40 45
 Pro Gly Leu Glu Asp Gly Thr His Trp Pro Tyr Ala Glu Leu Leu Ala
 50 55 60
 Gln Met Ser Val Leu Lys Lys Ser His Thr Ala Phe Leu Arg Thr Thr
 65 70 75 80
 Cys Pro Thr Asn Ser His Trp Cys Gly
 85

<210> 219

<211> 276

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (7)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 219

Arg Val Ile Arg Leu Thr Xaa Arg Ala Asn Trp Ser Ser Thr Ala Val
 1 5 10 15

Ala Ala Ala Leu Glu Leu Val Asp Pro Pro Gly Cys Arg Asn Ser Ala
 20 25 30

Arg Val Lys Tyr Cys Val Val Tyr Asp Asn Asn Ser Ser Thr Leu Glu
 35 40 45

Ile Leu Leu Lys Asp Asp Asp Asp Asp Ser Asp Ser Asp Gly Asp Gly
 50 55 60

Lys Asp Leu Val Pro Gln Ala Ala Ile Glu Tyr Gly Arg Ile Leu Thr
 65 70 75 80

Arg Leu Thr His His Pro Val Tyr Ile Leu Lys Gly Gly Tyr Glu Arg
 85 90 95

Phe Ser Gly Thr Tyr His Phe Leu Arg Thr Gln Lys Ile Ile Trp Met
 100 105 110

Pro Gln Glu Leu Asp Ala Phe Gln Pro Tyr Pro Ile Glu Ile Val Pro
 115 120 125

Gly Lys Val Phe Val Gly Asn Phe Ser Gln Ala Cys Asp Pro Lys Ile
 130 135 140

Gln Lys Asp Leu Lys Ile Lys Ala His Val Asn Val Ser Met Asp Thr
 145 150 155 160

Gly Pro Phe Phe Ala Gly Asp Ala Asp Lys Leu Leu His Ile Arg Ile
 165 170 175

Glu Asp Ser Pro Glu Ala Gln Ile Leu Pro Phe Leu Arg His Met Cys
 180 185 190
 His Phe Ile Glu Ile His His His Leu Gly Ser Val Ile Leu Ile Phe
 195 200 205
 Ser Thr Gln Gly Ile Ser Arg Ser Cys Ala Ala Ile Ile Ala Tyr Leu
 210 215 220
 Met His Ser Asn Glu Gln Thr Leu Gln Arg Ser Trp Ala Tyr Val Lys
 225 230 235 240
 Lys Cys Lys Asn Asn Met Cys Pro Asn Arg Gly Leu Val Ser Gln Leu
 245 250 255
 Leu Glu Trp Glu Lys Thr Ile Leu Gly Asp Ser Ile Thr Asn Ile Met
 260 265 270
 Asp Pro Leu Tyr
 275

<210> 220
 <211> 196
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (98)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 220
 Ile Arg His Glu Phe Thr Ser Glu Lys Ser Trp Lys Ser Ser Cys Asn
 1 5 10 15
 Glu Gly Glu Ser Ser Ser Thr Ser Tyr Met His Gln Arg Ser Pro Gly
 20 25 30
 Gly Pro Thr Lys Leu Ile Glu Ile Ile Ser Asp Cys Asn Trp Glu Glu
 35 40 45
 Asp Arg Asn Lys Ile Leu Ser Ile Leu Ser Gln His Ile Asn Ser Asn
 50 55 60
 Met Pro Gln Ser Leu Lys Val Gly Ser Phe Ile Ile Glu Leu Ala Ser
 65 70 75 80
 Gln Arg Lys Ser Arg Gly Glu Lys Asn Pro Pro Val Tyr Ser Ser Arg
 85 90 95
 Val Xaa Ile Ser Met Pro Ser Cys Gln Asp Gln Asp Asp Met Ala Glu
 100 105 110
 Lys Ser Gly Ser Glu Thr Pro Asp Gly Pro Leu Ser Pro Gly Lys Met
 115 120 125
 Glu Asp Ile Ser Pro Val Gln Thr Asp Ala Leu Asp Ser Val Arg Glu

130 135 140
 Arg Leu His Gly Gly Lys Gly Leu Pro Phe Tyr Ala Gly Leu Ser Pro
 145 150 155 160
 Ala Gly Lys Leu Val Ala Tyr Lys Arg Lys Pro Ser Ser Ser Thr Ser
 165 170 175
 Gly Leu Ile Gln Val Arg Ile Ile Phe Asn Leu Gly Ile Ala Pro Leu
 180 185 190
 Tyr Thr Pro Arg
 195

<210> 221
 <211> 24
 <212> PRT
 <213> Homo sapiens

<400> 221
 Cys Asn Ile Glu Tyr Ile Arg Ser Asp Lys Cys Met Phe Lys His Glu
 1 5 10 15
 Leu Glu Glu Leu Arg Thr Thr Ile
 20

<210> 222
 <211> 127
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (8)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (20)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (21)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (126)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 222
 His His Gln Gln Val Pro Glu Xaa Asp Arg Glu Asp Ser Pro Glu Arg
 1 5 10 15
 Cys Ser Asp Xaa Xaa Glu Glu Lys Lys Ala Arg Arg Gly Arg Ser Pro

			20						25									30
Lys	Gly	Glu	Phe	Lys	Asp	Glu	Glu	Glu	Thr	Val	Thr	Thr	Lys	His	Ile			
		35					40					45						
His	Ile	Thr	Gln	Ala	Thr	Glu	Thr	Thr	Thr	Thr	Arg	His	Lys	Arg	Thr			
	50					55					60							
Ala	Asn	Pro	Ser	Lys	Thr	Ile	Asp	Leu	Gly	Ala	Ala	Ala	His	Tyr	Thr			
65					70					75					80			
Gly	Asp	Lys	Ala	Ser	Pro	Asp	Gln	Asn	Ala	Ser	Thr	His	Thr	Pro	Gln			
				85					90					95				
Ser	Ser	Val	Lys	Thr	Ser	Val	Pro	Ser	Ser	Lys	Ser	Ser	Gly	Asp	Leu			
			100					105					110					
Val	Asp	Leu	Phe	Asp	Gly	Thr	Ser	Gln	Cys	Asn	Arg	Arg	Xaa	Ser				
		115					120					125						

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<210> 223
<211> 95
<212> PRT
<213> Homo sapiens
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<220>
<221> SITE
<222> (60)
<223> Xaa equals any of the naturally occurring L-amino acids
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<220>
<221> SITE
<222> (73)
<223> Xaa equals any of the naturally occurring L-amino acids
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<220>  
<221> SITE  
<222> (74)  
<223> Xaa equals any of the naturally occurring L-amino acids
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<400> 223
Val Ser Ser Asp Ser Val Gly Gly Phe Arg Tyr Ser Glu Arg Tyr Asp
 1          5          10          15
Pro Glu Pro Lys Ser Lys Trp Asp Glu Glu Trp Asp Lys Asn Lys Ser
      20          25          30
Ala Phe Pro Phe Ser Asp Lys Leu Gly Glu Leu Ser Asp Lys Ile Gly
      35          40          45
Ser Thr Ile Asp Asp Thr Ile Ser Lys Phe Arg Xaa Lys Ile Glu Lys
      50          55          60
Thr Leu Gln Lys Asp Ala Ala Thr Xaa Xaa Arg Lys Arg Lys Arg Glu
      65          70          75          80
Glu Ala Asp Leu Pro Lys Val Asn Ser Lys Met Lys Arg Arg Leu

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85

90

95

<210> 224

<211> 45

<212> PRT

<213> Homo sapiens

<400> 224

Arg Gln Ser Ile Phe Ile Ser His Arg Pro Gln Arg Pro Pro Gln Pro
1 5 10 15

Asp Thr Ser Ala Gln Gln Ile Leu Pro Lys Pro Leu Ile Leu Glu Gln
20 25 30

Gln His Ile Thr Gln Gly Thr Lys Gln Val Gln Ile Arg
35 40 45

<210> 225

<211> 190

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (72)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (163)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (180)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 225

Asp Gln Asp Gly Leu Arg Ala Val Ala Ala Leu Thr Leu His Gln Gly
1 5 10 15

Arg Gln Leu Leu Tyr Arg Lys Phe Val His Pro Ser Leu Ser Arg His
20 25 30

Glu Lys Glu Ile Asp Ala Tyr Ile Val Gln Ala Lys Glu Arg Ser Tyr
35 40 45

Glu Thr Val Leu Ser Phe Gly Lys Arg Gly Leu Asn Ile Ala Ala Ser
50 55 60

Ala Ala Val Gln Ala Ala Thr Xaa Ser Gln Gly Ala Leu Ala Gly Arg
65 70 75 80

Leu Arg Ser Phe Ser Met Gln Asp Leu Arg Ser Ile Ser Asp Ala Pro
85 90 95

Ala Pro Ala Tyr His Asp Pro Leu Tyr Leu Glu Asp Gln Val Ser His
 100 105 110

Arg Arg Pro Pro Ile Gly Tyr Arg Ala Gly Gly Leu Gln Asp Ser Asp
 115 120 125

Thr Glu Asp Glu Cys Trp Ser Asp Thr Glu Ala Val Pro Arg Ala Pro
 130 135 140

Ala Arg Pro Arg Glu Lys Pro Leu Ile Arg Ser Gln Ser Leu Arg Val
 145 150 155 160

Val Lys Xaa Lys Pro Pro Val Arg Glu Gly Thr Ser Arg Ser Leu Lys
 165 170 175

Val Arg Thr Xaa Lys Lys Thr Val Pro Ser Asp Val Asp Ser
 180 185 190

<210> 226

<211> 153

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (45)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (47)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (68)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (84)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (110)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

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<222> (120)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (149)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 226

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Leu Cys His Arg Leu Pro Gly Arg Leu Gln Leu Leu Gly Val Pro Val
 1              5              10              15

His Ala Gly Pro Leu Trp Val Tyr Ser Gly Leu Pro Gly Thr His Asp
      20              25              30

His Arg His Pro Pro Gly Leu Pro Arg Pro Leu Ala Xaa His Xaa Gly
      35              40              45

Pro Ala Leu His Gln His Trp Gly Pro Gly Ala Leu Gln Glu Ser Gln
      50              55              60

Ala Gly Gly Xaa Arg Arg Gly Pro Pro His Ser Gly Arg Tyr Leu Arg
      65              70              75              80

Asp Gly Gly Xaa Leu Leu Val Arg Phe Asn Ile Thr Arg Asp Phe Phe
      85              90              95

Asp Pro Leu Tyr Pro Gly Thr Lys Tyr Glu Leu Gly Pro Xaa Leu Tyr
      100              105              110

Leu Gly Trp Ser Ala Ser Leu Xaa Ser Ile Leu Gly Gly Leu Cys Leu
      115              120              125

Cys Ser Ala Cys Cys Cys Gly Ser Asp Glu Asp Gln Pro Pro Ala Pro
      130              135              140

Gly Gly Pro Thr Xaa Leu Pro Cys Pro
145              150

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<210> 227

<211> 33

<212> PRT

<213> Homo sapiens

<400> 227

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Val Asp Gln Met Phe Gln Phe Ala Ser Ile Asp Val Ala Gly Asn Leu
 1              5              10              15

Asp Tyr Lys Ala Leu Ser Tyr Val Ile Thr His Gly Glu Glu Lys Glu
      20              25              30

Glu

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<210> 228

<211> 15

<212> PRT

<213> Homo sapiens

<400> 228

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Ile Arg His Glu Ala Tyr Val Ile Leu Ala Val Cys Leu Gly Gly
 1              5              10              15

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<210> 229
 <211> 185
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (105)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 229
 Trp Ile Gln Arg Ile Arg His Glu Thr Asn Pro Lys Cys Ser Tyr Ile
 1 5 10 15
 Pro Pro Cys Lys Arg Glu Asn Gln Lys Asn Leu Glu Ser Val Met Asn
 20 25 30
 Trp Gln Gln Tyr Trp Lys Asp Glu Ile Gly Ser Gln Pro Phe Thr Cys
 35 40 45
 Tyr Phe Asn Gln His Gln Arg Pro Asp Asp Val Leu Leu His Arg Thr
 50 55 60
 His Asp Glu Ile Val Leu Leu His Cys Phe Leu Trp Pro Leu Val Thr
 65 70 75 80
 Phe Val Val Gly Val Leu Ile Val Val Leu Thr Ile Cys Ala Lys Ser
 85 90 95
 Leu Ala Val Lys Ala Glu Ala Met Xaa Glu Ala Gln Val Leu Leu Lys
 100 105 110
 Gly Lys Glu Ala Cys Arg Lys Gln Ser Thr Glu Ala Val Leu Ile Gly
 115 120 125
 Thr Arg Pro Pro Ala Glu Pro Val Phe Pro Gly Ala Gly Asp Gly Gln
 130 135 140
 Gly His Asp Arg Ala Leu Arg Gly Ser Ser Leu Ser Gly Asn Arg Asn
 145 150 155 160
 Arg His Asn Trp Lys Thr Trp Asn Leu Lys Ala Cys Ile Pro Ser Ala
 165 170 175
 Val Ala Met Ala Lys Gly Ser Arg Ser
 180 185

<210> 230
 <211> 152
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (21)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 230

His Tyr Glu Lys Val Arg Leu Gln Val Pro Ile Arg Asn Ser Arg Val
1 5 10 15

Asp Pro Arg Val Xaa Lys Phe Thr Ile Ser Asp His Pro Gln Pro Ile
20 25 30

Asp Pro Leu Leu Lys Asn Cys Ile Gly Asp Phe Leu Lys Thr Leu Glu
35 40 45

Asp Pro Asp Leu Asn Val Arg Arg Val Ala Leu Val Thr Phe Asn Ser
50 55 60

Ala Ala His Asn Lys Pro Ser Leu Ile Arg Asp Leu Leu Asp Thr Val
65 70 75 80

Leu Pro His Leu Tyr Asn Glu Thr Lys Val Arg Lys Glu Leu Ile Arg
85 90 95

Glu Val Glu Met Gly Pro Phe Lys His Thr Val Asp Asp Gly Leu Asp
100 105 110

Ile Arg Lys Ala Ala Phe Glu Cys Met Tyr Thr Leu Leu Asp Ser Cys
115 120 125

Leu Asp Arg Leu Asp Ile Phe Glu Phe Leu Asn His Val Glu Asp Gly
130 135 140

Leu Lys Asp His Tyr Asp Ile Lys
145 150

<210> 231

<211> 79

<212> PRT

<213> Homo sapiens

<400> 231

Ile Arg His Glu His Leu Arg Gly Val Gln Glu Arg Val Asn Leu Ser
1 5 10 15

Ala Pro Leu Leu Pro Lys Glu Asp Pro Ile Phe Thr Tyr Leu Ser Lys
20 25 30

Arg Leu Gly Arg Ser Ile Asp Asp Ile Gly His Leu Ile His Glu Gly
35 40 45

Leu Gln Lys Asn Thr Ser Ser Trp Val Leu Tyr Asn Met Ala Ser Phe
50 55 60

Tyr Trp Arg Ile Lys Asn Glu Pro Tyr Gln Val Val Glu Cys Ala
65 70 75

<210> 232

<211> 27

<212> PRT

<213> Homo sapiens

<400> 232

Glu Phe Gly Thr Ser Pro His Gln Thr Cys Gly Arg Arg Pro Gly Thr
1 5 10 15

Ala Ala Gly Trp Leu Leu Ala His Ser Thr Val
20 25

<210> 233

<211> 296

<212> PRT

<213> Homo sapiens

<400> 233

Asn Ser Ala Arg Asp Ser Leu Asn Thr Ala Ile Gln Ala Trp Gln Gln
1 5 10 15

Asn Lys Cys Pro Glu Val Glu Glu Leu Val Phe Ser His Phe Val Ile
20 25 30

Cys Asn Asp Thr Gln Glu Thr Leu Arg Phe Gly Gln Val Asp Thr Asp
35 40 45

Glu Asn Ile Leu Leu Ala Ser Leu His Ser His Gln Tyr Ser Trp Arg
50 55 60

Ser His Lys Ser Pro Gln Leu Leu His Ile Cys Ile Glu Gly Trp Gly
65 70 75 80

Asn Trp Arg Trp Ser Glu Pro Phe Ser Val Asp His Ala Gly Thr Phe
85 90 95

Ile Arg Thr Ile Gln Tyr Arg Gly Arg Thr Ala Ser Leu Ile Ile Lys
100 105 110

Val Gln Gln Leu Asn Gly Val Gln Lys Gln Ile Ile Ile Cys Gly Arg
115 120 125

Gln Ile Ile Cys Ser Tyr Leu Ser Gln Ser Ile Glu Leu Lys Val Val
130 135 140

Gln His Tyr Ile Gly Gln Asp Gly Gln Ala Val Val Arg Glu His Phe
145 150 155 160

Asp Cys Leu Thr Ala Lys Gln Lys Leu Pro Ser Tyr Ile Leu Glu Asn
165 170 175

Asn Glu Leu Thr Glu Leu Cys Val Lys Ala Lys Gly Asp Glu Asp Trp
180 185 190

Ser Arg Asp Val Cys Leu Glu Ser Lys Ala Pro Glu Tyr Ser Ile Val
195 200 205

Ile Gln Val Pro Ser Ser Asn Ser Ser Ile Ile Tyr Val Trp Cys Thr
210 215 220

Val Leu Thr Leu Glu Pro Asn Ser Gln Val Gln Gln Arg Met Ile Val
225 230 235 240

Phe Ser Pro Leu Phe Ile Met Arg Ser His Leu Pro Asp Pro Ile Ile
245 250 255

Ile His Leu Glu Lys Arg Ser Leu Gly Leu Ser Glu Thr Gln Ile Ile
260 265 270

Pro Gly Lys Gly Gln Glu Lys Pro Leu Gln Asn Ile Glu Pro Asp Leu
275 280 285

Val His His Leu Thr Phe Gln Ala
290 295

<210> 234

<211> 26

<212> PRT

<213> Homo sapiens

<400> 234

Asn Lys Cys Pro Glu Val Glu Glu Leu Val Phe Ser His Phe Val Ile
1 5 10 15

Cys Asn Asp Thr Gln Glu Thr Leu Arg Phe
20 25

<210> 235

<211> 25

<212> PRT

<213> Homo sapiens

<400> 235

His Ile Cys Ile Glu Gly Trp Gly Asn Trp Arg Trp Ser Glu Pro Phe
1 5 10 15

Ser Val Asp His Ala Gly Thr Phe Ile
20 25

<210> 236

<211> 27

<212> PRT

<213> Homo sapiens

<400> 236

Val Val Arg Glu His Phe Asp Cys Leu Thr Ala Lys Gln Lys Leu Pro
1 5 10 15

Ser Tyr Ile Leu Glu Asn Asn Glu Leu Thr Glu
20 25

<210> 237

<211> 27

<212> PRT

<213> Homo sapiens

<400> 237

Glu Asp Trp Ser Arg Asp Val Cys Leu Glu Ser Lys Ala Pro Glu Tyr
1 5 10 15

Ser Ile Val Ile Gln Val Pro Ser Ser Asn Ser
20 25

<210> 238

<211> 27

<212> PRT

<213> Homo sapiens

<400> 238

Ile Ile His Leu Glu Lys Arg Ser Leu Gly Leu Ser Glu Thr Gln Ile
1 5 10 15

Ile Pro Gly Lys Gly Gln Glu Lys Pro Leu Gln
20 25

<210> 239

<211> 162

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (44)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (47)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (60)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (63)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (64)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 239

Leu Ile Ile Gln Asp Gln Thr Arg Arg Cys His Gly Leu Trp His Leu
1 5 10 15

Pro Ser Leu Leu Trp Pro Leu Leu Trp Ser Ser Gly Thr Gly Leu Cys

	20		25		30										
Arg	Asn	Val	Cys	Arg	Leu	His	Gly	Ile	Tyr	His	Xaa	Val	Leu	Xaa	Arg
	35						40					45			
Val	Gly	His	Ala	Tyr	Gln	Thr	Ser	Phe	Arg	Gln	Xaa	Val	Cys	Xaa	Xaa
	50					55					60				
Trp	Ala	Ala	Asp	Leu	Cys	Gly	Arg	His	Glu	Glu	Gly	Ile	Ile	Glu	Asn
65					70					75					80
Thr	Tyr	Arg	Leu	Ser	Cys	Asn	His	Val	Phe	His	Glu	Phe	Cys	Ile	Arg
				85					90					95	
Gly	Trp	Cys	Ile	Val	Gly	Lys	Lys	Gln	Thr	Cys	Pro	Tyr	Cys	Lys	Glu
			100					105						110	
Lys	Val	Asp	Leu	Lys	Arg	Met	Phe	Ser	Asn	Pro	Trp	Glu	Arg	Pro	His
		115					120						125		
Val	Met	Tyr	Gly	Gln	Leu	Leu	Asp	Trp	Leu	Arg	Tyr	Leu	Val	Ala	Trp
	130					135					140				
Gln	Pro	Val	Ile	Ile	Gly	Val	Val	Gln	Gly	Ile	Asn	Tyr	Ile	Leu	Gly
145					150					155					160
Leu	Glu														

<210> 240

<211> 164

<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (95)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (97)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (111)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (114)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 240

Thr	Ala	Phe	Val	Thr	Phe	Arg	Ala	Thr	Arg	Lys	Pro	Leu	Val	Gln	Thr
1				5					10					15	

Thr Pro Arg Leu Val Tyr Lys Trp Phe Leu Leu Ile Tyr Lys Ile Ser
 20 25 30
 Tyr Ala Thr Gly Ile Val Gly Tyr Met Ala Val Met Phe Thr Leu Phe
 35 40 45
 Gly Leu Asn Leu Leu Phe Lys Ile Lys Pro Glu Asp Ala Met Asp Phe
 50 55 60
 Gly Ile Ser Leu Leu Phe Tyr Gly Leu Tyr Tyr Gly Val Leu Glu Arg
 65 70 75 80
 Asp Phe Ala Glu Met Cys Ala Asp Tyr Met Ala Ser Thr Ile Xaa Phe
 85 90 95
 Xaa Ser Glu Ser Gly Met Pro Thr Lys His Leu Ser Asp Ser Xaa Cys
 100 105 110
 Ala Xaa Cys Gly Gln Gln Ile Phe Val Asp Val Met Lys Arg Gly Ser
 115 120 125
 Leu Arg Thr Arg Ile Gly Cys Pro Ala Ile Met Ser Ser Thr Ser Ser
 130 135 140
 Ala Ser Val Ala Gly Ala Ser Trp Glu Arg Ser Lys Arg Val Pro Thr
 145 150 155 160
 Ala Lys Arg Arg

<210> 241
 <211> 28
 <212> PRT
 <213> Homo sapiens

<400> 241
 Ala Thr Ser Met Lys Arg Leu Ser His Pro Ser Ile Cys Arg Thr Gly
 1 5 10 15
 Leu Pro Leu Ser Gln Gln Lys Arg Ala Ser Leu Leu
 20 25

<210> 242
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 242
 Met Ile Ile Leu Ser Cys Cys Ser Leu Trp Ile Tyr Asp Tyr Leu Ile
 1 5 10 15
 His Pro Val Pro Ser Val Gly His Arg Val Cys Leu Cys Cys Leu Pro
 20 25 30
 Glu Ser Ala Thr Gly Arg Ile Ser Pro Leu Gly Glu Gly Pro Arg Lys

35 40 45
 Trp His Gly Leu Arg Arg Ser Pro Glu His Ile Ser Leu Gly Gly Leu
 50 55 60
 Leu Leu Ser Ser Arg Leu Met Ala Phe Cys Asn Leu Ser Arg Ala Val
 65 70 75 80
 Leu Pro Gly Asn Arg Thr Met Glu Thr Glu Thr Tyr Gln Leu Trp Ala
 85 90 95
 Ser Gln Tyr Gln Arg Lys Trp Val Ser Arg Ser Leu Ser Gln Val Gln
 100 105 110
 Cys Leu Arg Leu
 115

<210> 243
 <211> 149
 <212> PRT
 <213> Homo sapiens

<220>
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 <222> (128)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (133)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<220>
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 <222> (143)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 243
 Trp Ile Pro Arg Ala Ala Gly Ile Arg His Glu His Leu Ser Thr Leu
 1 5 10 15
 Asp Arg Ser Val Ile Trp Ser Lys Ser Ile Leu Asn Ala Arg Cys Lys
 20 25 30
 Ile Cys Arg Lys Lys Gly Asp Ala Glu Asn Met Val Leu Cys Asp Gly
 35 40 45

Cys Asp Arg Gly His His Thr Tyr Cys Val Arg Pro Lys Leu Lys Thr
 50 55 60
 Val Pro Glu Gly Asp Trp Phe Cys Pro Glu Cys Arg Pro Lys Gln Arg
 65 70 75 80
 Ser Arg Arg Leu Ser Ser Arg Gln Arg Pro Ser Leu Glu Ser Asp Glu
 85 90 95
 Asp Val Glu Asp Ser Met Gly Gly Glu Asp Asp Glu Val Asp Gly Asp
 100 105 110
 Glu Glu Glu Gly Gln Ser Glu Glu Glu Glu Tyr Glu Val Glu Gln Xaa
 115 120 125
 Glu Asp Asp Ser Xaa Glu Glu Xaa Glu Val Arg Xaa Val Leu Xaa Cys
 130 135 140
 Asn Lys Met Ser Gln
 145

<210> 244
 <211> 11
 <212> PRT
 <213> Homo sapiens

<400> 244
 Met Arg Val Ala Arg Tyr Val Glu Arg Lys Ala
 1 5 10

<210> 245
 <211> 183
 <212> PRT
 <213> Homo. sapiens

<220>
 <221> SITE
 <222> (29)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
 <221> SITE
 <222> (31)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
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 <222> (87)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>
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 <222> (89)
 <223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (159)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 245

Gln Arg Trp Leu Lys His Gly Ala Asn Gln Cys Lys Phe Glu His Asn
 1 5 10 15

Asp Cys Leu Asp Lys Ser Tyr Lys Cys Tyr Ala Ala Xaa Glu Xaa Val
 20 25 30

Gly Glu Asn Ile Trp Leu Gly Gly Ile Lys Ser Phe Thr Pro Arg His
 35 40 45

Ala Ile Thr Ala Trp Tyr Asn Glu Thr Gln Phe Tyr Asp Phe Asp Ser
 50 55 60

Leu Ser Cys Ser Arg Val Cys Gly His Tyr Thr Gln Leu Val Trp Ala
 65 70 75 80

Asn Ser Phe Tyr Val Gly Xaa Ala Xaa Ala Met Cys Pro Asn Leu Gly
 85 90 95

Gly Ala Ser Thr Ala Ile Phe Val Cys Asn Tyr Gly Pro Ala Gly Asn
 100 105 110

Phe Ala Asn Met Pro Pro Tyr Val Arg Gly Glu Ser Cys Ser Leu Cys
 115 120 125

Ser Lys Glu Glu Lys Cys Val Lys Asn Leu Cys Lys Asn Pro Phe Leu
 130 135 140

Lys Pro Thr Gly Arg Ala Pro Gln Gln Thr Ala Phe Asn Pro Xaa Gln
 145 150 155 160

Leu Arg Phe Ser Ser Ser Glu Asn Leu Leu Met Ser Phe Ile Tyr Lys
 165 170 175

Arg Asn Ser Gln Met Leu Lys
 180

<210> 246

<211> 164

<212> PRT

<213> Homo sapiens

<400> 246

Thr Glu Gly Gly Cys Ala Leu Val Pro Asn Asp Met Glu Ser Leu Lys
 1 5 10 15

Gln Lys Leu Val Arg Val Leu Glu Glu Asn Leu Ile Leu Ser Glu Lys
 20 25 30

Ile Gln Gln Leu Glu Glu Gly Ala Ala Ile Ser Ile Val Ser Gly Gln
 35 40 45

Gln Ser His Thr Tyr Asp Asp Leu Leu His Lys Asn Gln Gln Leu Thr

50	55	60
Met Gln Val Ala Cys Leu Asn Gln Glu Leu Ala Gln Leu Lys Lys Leu		
65	70	75 80
Glu Lys Thr Val Ala Ile Leu His Glu Ser Gln Arg Ser Leu Val Val		
	85	90 95
Thr Asn Glu Tyr Leu Leu Gln Gln Leu Asn Lys Glu Pro Lys Gly Tyr		
	100	105 110
Ser Gly Lys Ala Leu Leu Pro Pro Glu Lys Gly His His Leu Gly Arg		
	115	120 125
Ser Ser Pro Phe Gly Lys Ser Thr Leu Ser Ser Ser Ser Pro Val Ala		
	130	135 140
His Glu Thr Gly Gln Tyr Leu Ile Gln Ser Val Leu Asp Ala Ala Pro		
145	150	155 160
Glu Pro Gly Leu		

<210> 247
 <211> 5
 <212> PRT
 <213> Homo sapiens

<400> 247
 Ser Met Val Ser Lys
 1 5

<210> 248
 <211> 50
 <212> PRT
 <213> Homo sapiens

<220>
 <221> SITE
 <222> (34)
 <223> Xaa equals any of the naturally occurring L-amino acids

<400> 248
 Asn Thr Asp Trp Asp Gln Thr Val Leu Ile Val Leu Arg Ile Ser Ser
 1 5 10 15

Thr Leu Pro Val Ala Leu Leu Arg Asp Glu Val Pro Gly Trp Phe Leu
 20 25 30

Lys Xaa Pro Glu Pro Gln Leu Ile Ser Lys Glu Leu Ile Met Leu Thr
 35 40 45

Glu Val
 50

<210> 249
<211> 44
<212> PRT
<213> Homo sapiens

<400> 249
Val Ala Glu Ser Thr Glu Glu Pro Ala Gly Ser Asn Arg Gly Gln Tyr
1 5 10 15
Pro Glu Asp Ser Ser Ser Asp Gly Leu Arg Gln Arg Glu Val Leu Arg
20 25 30
Asn Leu Ser Ser Pro Gly Trp Glu Asn Ile Ser Arg
35 40

<210> 250
<211> 30
<212> PRT
<213> Homo sapiens

<400> 250
Ala Arg Glu Pro Leu Gly Leu Thr Gln Asp Pro Leu Val Phe Gly Met
1 5 10 15
Thr Ser Phe Leu Gln Thr Ser Ser Pro Ile Pro Asn Ser Cys
20 25 30

<210> 251
<211> 15
<212> PRT
<213> Homo sapiens

<400> 251
Phe Gln Ala Pro Ala Ser Ala Arg Thr Ala Cys Ser Thr Leu Leu
1 5 10 15

<210> 252
<211> 37
<212> PRT
<213> Homo sapiens

<400> 252
Ala Gln Pro Ser Pro Cys Pro Ser Cys Leu Ala His Ser Trp Pro Pro
1 5 10 15
Phe Arg Leu Leu Ser Leu Pro Pro Pro Ala Gly Ala Ser Leu Gly Asp
20 25 30
Gly Arg Val Cys Ser
35

<210> 253
<211> 121
<212> PRT

<213> Homo sapiens

<220>

<221> SITE

<222> (43)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (104)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE

<222> (115)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 253

His Ser Leu Pro Pro Ala Leu Pro Ala Trp Leu Thr Pro Gly His Pro
1 5 10 15

Ser Asp Ser Ser Leu Cys Leu Leu Gln Leu Ala Pro His Leu Val Met
20 25 30

Ala Val Ser Val Pro Trp Pro Leu Pro Glu Xaa Leu Gly Phe Ser Cys
35 40 45

Cys His Cys Val Ser Leu Thr Gly Pro His Ala Gly Phe Ser Tyr His
50 55 60

Phe Leu His Pro Ala Glu Pro Arg Ala Trp Gln His Gln Ser Ser Val
65 70 75 80

Val Gly Met Ser Arg Lys Gln Ala Ser Phe Ser Met Ala Gln Lys Gly
85 90 95

Val Cys His Leu Gly Lys Ser Xaa Lys Arg Gly Ser Lys Lys Ala Ser
100 105 110

Cys Pro Xaa Tyr Pro Ser Phe Ser Lys
115 120

<210> 254

<211> 24

<212> PRT

<213> Homo sapiens

<400> 254

Ile Gly Ile Arg Val Trp Tyr Tyr Arg Asn Gln Lys Asn Ser Lys Gln
1 5 10 15

Met Trp Ile Lys Cys Leu Gly Ser
20

Applicant's or agent's file
reference number

PZ017PCT

International application no.

PCT/US 98/20775

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>125</u> , line <u>7</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution American Type Culture Collection ("ATCC")	
Address of depositary institution (including postal code and country) 10801 University Boulevard Manassas, Virginia 20110-2209 United States of America	
Date of deposit 28 AUGUST 1997	Accession Number 209225
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g., "Accession Number of Deposit")	

For receiving Office use only
<input checked="" type="checkbox"/> This sheet was received with the international application
Authorized officer <i>Sonya D. Barnes</i>

For International Bureau use only
<input type="checkbox"/> This sheet was received by the International Bureau on:
Authorized officer

Form PCT/RO/134 (July 1992)

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner. the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

AUSTRALIA

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

Page 2

DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

SWEDEN

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by a applicant in the individual case.

NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/20775

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : Please See Extra Sheet.
US CL : Please See Extra Sheet.
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/23.5, 23.1; 435/320.1, 440, 252.3, 69.1, 6, 7.1; 530/324, 387.1; 436/501

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Please See Extra Sheet.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WILSON et al, 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans, Nature. 03 March 1994, Vol. 368, No. 6466, pages 32-38, see entire document.	1 and 7-10

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:	*T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
A document defining the general state of the art which is not considered to be of particular relevance	*X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
B earlier document published on or after the international filing date	*Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*A* document member of the same patent family
O document referring to an oral disclosure, use, exhibition or other means	
P document published prior to the international filing date but later than the priority date claimed	

Date of the actual completion of the international search

18 DECEMBER 1998

Date of mailing of the international search report

26 JAN 1999

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231

Facsimile No. (703) 305-3230

Authorized officer

JAMES MARTINELL

Telephone No. (703) 308-0196

Form PCT/ISA/210 (second sheet)(July 1992)*

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/20775

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☒ Claims Nos.: 23
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

Claim 23 is directed to a product produced by the method of claim 20. Claim 20 is a method of identification and no product is produced by that method. Hence, no meaningful search can be made of claim 23.

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

Form PCT/ISA/210 (continuation of first sheet(1))(July 1992)*

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/20775

A. CLASSIFICATION OF SUBJECT MATTER: IPC (6):

C12N 15/12, 15/00, 15/11, 15/63; A61K 38/16; C07K 16/00; C12P 21/02; C12Q 1/68; G01N 33/53, 33/68

A. CLASSIFICATION OF SUBJECT MATTER: US CL :

536/23.5, 23.1; 435/320.1, 440, 252.3, 69.1, 6, 7.1; 530/324, 387.1; 436/501

B. FIELDS SEARCHED

Electronic data bases consulted (Name of data base and where practicable terms used):

MPSRCH (SEQ ID NOs 11 and 113 only). One nucleotide sequence and one amino acid sequence have been searched. It is not clear which sequences are embraced by the claims because the claims refer to sequences X and Y. The table at pages 125-137 contains many sequences X and Y, yet the claims refer to X and Y in the singular only. If the claims are to embrace more than one X and more than one Y, it is not clear whether each X sequence always requires the corresponding sequence Y (e.g., see claim 1(a) and (c)). Additionally, the claims are in improper form in referring to the description (see PCT Rule 6.2(a)). Accordingly, the first X nucleotide sequence disclosed and the first Y amino acid sequence disclosed in the Table on pages 125-137 were searched.